

Thu Nov 18 16:38:24 2004

Search #3

seq1.rag

No body, the open ended w/ X goes page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 ; Search time 67 seconds

(without alignments)  
42.833 Million cell updates/sec

Title: SEQ1

Perfect score: 51

Sequence: 1 xcykwvct 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 356729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004as:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID      | Description |
|------------|-------|-------------|--------|------------|-------------|
| 1          | 51    | 100.0       | 8      | 1 AAB61464 | Cyclic oc   |
| 2          | 51    | 100.0       | 8      | 1 AAP71379 | Sequence    |
| 3          | 51    | 100.0       | 8      | 1 AAP71378 | Sequence    |
| 4          | 51    | 100.0       | 8      | 1 AAR07024 | Sequence    |
| 5          | 51    | 100.0       | 8      | 1 AAR07021 | Sequence    |
| 6          | 51    | 100.0       | 8      | 1 AAR07022 | Sequence    |
| 7          | 51    | 100.0       | 8      | 1 AAR05192 | Sequence    |
| 8          | 51    | 100.0       | 8      | 1 AAR14234 | Sequence    |
| 9          | 51    | 100.0       | 8      | 1 AAR14226 | Sequence    |
| 10         | 51    | 100.0       | 8      | 1 AAR10504 | Sequence    |
| 11         | 51    | 100.0       | 8      | 1 AAR26371 | Sequence    |
| 12         | 51    | 100.0       | 8      | 1 AAR26370 | Sequence    |
| 13         | 51    | 100.0       | 8      | 1 AAR27177 | Sequence    |
| 14         | 51    | 100.0       | 8      | 1 AAR27178 | Sequence    |
| 15         | 51    | 100.0       | 8      | 1 AAR27188 | Sequence    |
| 16         | 51    | 100.0       | 8      | 1 AAR27190 | Sequence    |
| 17         | 51    | 100.0       | 8      | 1 AAR23951 | Sequence    |
| 18         | 51    | 100.0       | 8      | 1 AAR40816 | Sequence    |
| 19         | 51    | 100.0       | 8      | 1 AAR41505 | Sequence    |
| 20         | 51    | 100.0       | 8      | 1 AAR41501 | Sequence    |
| 21         | 51    | 100.0       | 8      | 1 AAR31510 | Sequence    |
| 22         | 51    | 100.0       | 8      | 1 AAR42656 | Sequence    |
| 23         | 51    | 100.0       | 8      | 1 AAR56780 | Sequence    |
| 24         | 51    | 100.0       | 8      | 1 AAR56809 | Sequence    |
| 25         | 51    | 100.0       | 8      | 1 AAR56778 | Sequence    |

# ALIGNMENTS

|    |    |       |   |            |           |
|----|----|-------|---|------------|-----------|
| 26 | 51 | 100.0 | 8 | 2 AAR56806 | Somatosta |
| 27 | 51 | 100.0 | 8 | 2 AAR55721 | Somatosta |
| 28 | 51 | 100.0 | 8 | 2 AAR50280 | Somatosta |
| 29 | 51 | 100.0 | 8 | 2 AAR85726 | Somatosta |
| 30 | 51 | 100.0 | 8 | 2 AAR76204 | Somatosta |
| 31 | 51 | 100.0 | 8 | 2 AAR85569 | Somatosta |
| 32 | 51 | 100.0 | 8 | 2 AAR85573 | Somatosta |
| 33 | 51 | 100.0 | 8 | 2 AAR81656 | Somatosta |
| 34 | 51 | 100.0 | 8 | 2 AAR81649 | Somatosta |
| 35 | 51 | 100.0 | 8 | 2 AAR92931 | Somatosta |
| 36 | 51 | 100.0 | 8 | 2 AAW48641 | Somatosta |
| 37 | 51 | 100.0 | 8 | 2 AAW18453 | Somatosta |
| 38 | 51 | 100.0 | 8 | 2 AAW68221 | Somatosta |
| 39 | 51 | 100.0 | 8 | 2 AAW6749  | Somatosta |
| 40 | 51 | 100.0 | 8 | 2 AAW50948 | Somatosta |
| 41 | 51 | 100.0 | 8 | 2 AAW51864 | Somatosta |
| 42 | 51 | 100.0 | 8 | 2 AAW51667 | Somatosta |
| 43 | 51 | 100.0 | 8 | 2 AAW51860 | Somatosta |
| 44 | 51 | 100.0 | 8 | 2 AAY22061 | Somatosta |
| 45 | 51 | 100.0 | 8 | 2 AAY22109 | Somatosta |

|          |   |                          |
|----------|---|--------------------------|
| RESULT 1 | AAB61464  | standard; protein; 8 AA. |
| ID       | AAB61464  |                          |
| AC       | AAB61464  |                          |
| XX       | 25-MAR-2003 (revised)   |                          |
| DT       | 27-OCT-1991 (first entry)   |                          |
| DE       | Cyclic octapeptide somatostatin analogue.                                 |                          |
| XX       | Growth hormone; prolactin; insulin; glucagon; gastrin; secretin;          |                          |
| KW       | Cholecystokinin.  |                          |
| XX       | Synthetic.  |                          |
| OS       |   |                          |
| XX       | Key   | Location/Qualifiers      |
| XX       | Modified-site   | 1 /label= D-Phe          |
| FT       | Disulfide-bond  | 2 . 7                    |
| FT       | Modified-site   | 4 /label= D-Tyr          |
| XX       |   |                          |
| PN       | EP203031-A.   |                          |
| XX       | 26-NOV-1986.  |                          |
| PD       |   |                          |
| XX       | 15-APR-1986; 86EP-00810174.   |                          |
| PF       | 25-APR-1986; 85US-00727105.   |                          |
| XX       | PR 28-MAR-1986; 86US-00843539.  |                          |
| XX       | (TULANE ) TULANE EDUCATIONAL FUND.  |                          |
| PA       | Schally AV, Cai RZ;   |                          |
| PI       | WPI, 1986-313466/48.  |                          |
| XX       |   |                          |
| DR       | New cyclic octapeptide somatostatin analogues - and reduced linear        |                          |
| PT       | intermediates.  |                          |
| XX       | Claim 8; Page 31, 33pp, English.  |                          |
| PS       | Somatostatin analogues inhibit the release of growth hormone, prolactin,  |                          |
| XX       | insulin, glucagon, gastrin, secretin and cholecystokinin. They also       |                          |
| CC       | diminish gastrin stimulated secretion of gastric acid, and may be used in |                          |
| CC       | treatment of diabetic retinopathy, diabetes, ulcers, acute pancreatitis   |                          |
| CC       | and agromegaly. The analogues may also be used in treating prostatic      |                          |

|             |   |
|-------------|---|
| CC          | adeno-carcinomas, mammary carcinomas, insulinomas, gastrinomas and growth hormone and insulin dependent tumours. (Updated on 25-MAR-2003 to correct PA field.)  |
| CC          | PA field.)  |
| CC          | Sequence 8 AA;  |
| SQ          |   |
| OY          | 1 XCWKVCT 8<br>:     <br>Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;   |
| D6          | 1 FCWKVCT 8   |
| RESULT 2    |   |
| AAP71379    |   |
| ID          | AAP71379 standard; peptide; 8 AA.   |
| XX          |   |
| XX          | AAP71379;   |
| AC          |   |
| DT          | 09-SEP-2004 (revised)   |
| DT          | 25-MAR-2003 (revised)   |
| DT          | 03-OCT-2002 (revised)   |
| DT          | 03-MAY-1991 (first entry)   |
| XX          |   |
| DE          | Sequence of somatostatin analogue.  |
| XX          |   |
| KW          | Growth hormone secretion inhibitor; cancer therapy; Alzheimer's disease; diabetes.  |
| XX          |   |
| OS          | Synthetic.  |
| XX          |   |
| FT          | Key Location/Qualifiers   |
| FT          | Misc-difference 1 /label= pentafluoro-D-Phe   |
| FT          | Misc-difference 4 /label= D-Trp   |
| FT          | Misc-difference 8 /label= Thr-NH2   |
| EP214872-A. |   |
| PN          |   |
| PD          | 18-MAR-1987.  |
| XX          |   |
| Pf          | 12-SEP-1986; 86EP-00307044.   |
| PR          | 12-SEP-1985; 85US-00775488.   |
| PR          | 17-JUN-1986; 86US-00675266.   |
| PR          | 22-JUN-1988; 88US-00203883.   |
| PA          | (TULA ) TULANE EDUCATIONAL FUND FUND.   |
| XX          |   |
| PI          | Coy DH, Murphy WA, Heman ML;  |
| DR          | WPI; 1987-074173/11.  |
| XX          |   |
| PT          | Somatostatin analogue octa-peptide(s) with enhanced activity - are useful in the redn. of growth hormone, insulin glucagon, or pancreatic exocrine secretion, and have anticancer activity.   |
| PS          | Disclosure; Page; 10pp; English.  |
| CC          | Cpds. confg. the claimed peptides can be used instead of somatostatin. They are administered in somatostatin dosages or because of their greater potency, in smaller dosages. Dosage is 0.01-1000 mcg./kg./day pref. 0.1-100 mcg./kg./day to mammal eg human. (updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) |
| CC          | Revised record issued on 09-SEP-2004 : Correction to sequence location Sequence 8 AA,   |

```

Query Match      100.0%; Score 51; DB 1; Length 8;
Best Local Similarity 87.5%; Pred.No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 XCYMKVCT 8
           : |||||
           : |||||
Db          1 FCYMKVCT 8

RESULT 3
AAF71378
ID AAF71378 standard; peptide; 8 AA.
XX
AC AAF71378;
XX
DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 03-MAY-1991 (first entry)
XX
DE Sequence of somatostatin analogue.
XX
KM Growth hormone secretion inhibitor; cancer therapy; Alzheimer's disease;
KM diabetes.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label= D-beta-Nal
FT FT Misc-difference 4 /label= D-Trip
FT FT Misc-difference 8 /label= Thr-NH2
XX
PN EP214872-A.
XX
PD 18-MAR-1987.
XX
PF 12-SEP-1986; 86EP-00307044.
XX
PR 12-SEP-1985; 85US-00775488.
PR 17-JUN-1986; 86US-00875266.
PR 22-JUN-1988; 88US-00209883.
XX
PA (TULSA ) TULANE EDUCATIONAL FUND FUND.
XX
PI Coy DH, Murphy WA, Heman ML;
XX
DR WPI; 1987-074173/11.
XX
PT Somatostatin analogue octa-peptide(s) with enhanced activity - are useful
PT in the rean. of growth hormone, insulin glucagon, or pancreatic exocrine
PT secretion, and have anticancer activity.
XX
PS Disclosure; Page; 10pp; English.
XX
CC Cpls. contg. the claimed peptides can be used instead of somatostatin.
CC They are administered in somatostatin dosages or because of their greater
CC potency, in smaller dosages. Dosage is 0.01-1000 mcg./kg./day pref. 0.1-
CC 100 mcg./kg./day to mammal eg human. (Updated on 03-OCT-2002 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
CC
CC Revised record issued on 09-SEP-2004 : Correction to sequence location
XX
SQ Sequence 8 AA;

Query Match      100.0%; Score 51; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      1 XCYWKVCT 8
DB      1 XCYWKVCT 8

RESULT 4
AA07024 ID AAR07024 standard; protein; 8 AA.
AC AAR07024;
XX
XX 21-JAN-1991 (first entry)
XX
DE Octapeptide somatostatin analogue.
XX
XX Growth hormone dependent cancer; diabetes; Alzheimers disease; Cirrhosis;
XX hepatitis; insulin; glucagon.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /label= OTHER, Dextrorotatory
FT /note= "N-Ac-D-beta-Nal"
FT Modified-site 3
FT /label= Iodinated phenyl ring
FT Modified-site 4
FT /label= Dextrorotatory
PN EP389180-A.
XX
PD 26-SEP-1990.
XX
PF 15-MAR-1990; 90EP-00302760.
XX
PR 15-MAR-1989; 89US-00323777.
XX
XX (BIOM-) BIOMEASURE INC.
PA
XX Eck CR, Moreau S;
PI
DR WPI; 1990-292105/39.
XX
XX New octa:peptide somatostatin analogues - useful for treating diabetes,
XX liver disease, growth hormone dependent cancer, alzheimers disease etc.
XX
XX Claim 5; Page 5; 8pp; English.
XX
XX Analogues to somatostatin, useful for reducing or inhibiting release of
XX antagonising growth hormone, insulin, glucagon or pancreatic exocrine
XX solution. The peptides can treat diabetes related retinopathy, cirrhosis,
XX hepatitis, Alzheimer's disease, cancers etc
XX
XX Sequence 8 AA;
SO

Query Match 100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 XCYWKVCT 8
DB      1 XCYWKVCT 8

RESULT 5
AA07021 ID AAR07021 standard; protein; 8 AA.
XX
XX AAR07021;
XX
XX 21-JAN-1991 (first entry)
XX
XX Octapeptide somatostatin analogue.
DE

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XX      XX Growth hormone dependent cancer; diabetes; Alzheimers disease; Cirrhosis;
XX      XX hepatitis; insulin; glucagon.
XX      XX Synthetic.
XX      XX
XX      XX Key Location/Qualifiers
FH      FH Modified-site 1
FT      FT /label= OTHER, Dextrorotatory
FT      FT /note= "D-beta-Nal"
FT      FT Modified-site 3
FT      FT /label= Iodinated phenyl ring
FT      FT Modified-site 4
FT      FT /label= Dextrorotatory
PN      PN EP389180-A.
XX      XX
XX      XX 26-SEP-1990.
XX      XX
XX      XX 15-MAR-1990; 90EP-00302760.
XX      XX
XX      XX 15-MAR-1989; 89US-00323777.
XX      XX
XX      XX (BIOM-) BIOMEASURE INC.
PA      PA
XX      XX Eck CR, Moreau S;
PI      PI
XX      XX WPI; 1990-292105/39.
XX      XX
XX      XX New octa:peptide somatostatin analogues - useful for treating diabetes,
XX      XX liver disease, growth hormone dependent cancer, alzheimers disease etc.
XX      XX
XX      XX Claim 5; Page 5; 8pp; English.
XX      XX
XX      XX Analogues to somatostatin, useful for reducing or inhibiting release of
XX      XX antagonising growth hormone, insulin, glucagon or pancreatic exocrine
XX      XX solution. The peptides can treat diabetes related retinopathy, cirrhosis,
XX      XX hepatitis, Alzheimer's disease, cancers etc
XX      XX
XX      XX Sequence 8 AA;
SO

Query Match 100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 XCYWKVCT 8
DB      1 XCYWKVCT 8

RESULT 6
AA07022 ID AAR07022 standard; protein; 8 AA.
XX
XX AAR07022;
XX
XX 21-JAN-1991 (first entry)
XX
XX Octapeptide somatostatin analogue.
XX
XX Growth hormone dependent cancer; diabetes; Alzheimers disease; Cirrhosis;
XX hepatitis; insulin; glucagon.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH      FH Modified-site 1
FT      FT /label= Dextrorotatory
FT      FT /note= "Pentafluoro-D-Phe"
FT      FT Modified-site 3
FT      FT /label= Iodinated phenyl ring
FT      FT Modified-site 4
FT      FT /label= Dextrorotatory

```

XX EP389180-A.  
XX 26-SEP-1990.  
XX 15-MAR-1990; 90BP-00302760.  
XX 15-MAR-1989; 89US-00323777.  
XX (BIOM-) BIOMEASURE INC.  
XX Eck CR, Moreau S;  
XX WPI; 1990-292105/39.  
XX  
XX New octa-peptide somatostatin analogues - useful for treating diabetes,  
XX liver disease, growth hormone dependent cancer, alzheimers disease etc.  
XX  
XX Claim 5; Page 5; 8pp; English.  
XX  
XX Analogues to somatostatin, useful for reducing or inhibiting release of  
XX antagonising growth hormone, insulin, glucagon or pancreatic exocrine  
XX solution. The peptides can treat diabetes related retinopathy, cirrhosis,  
XX hepatitis, Alzheimer's disease, cancers etc  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 100.0%; Score 51; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 XCYWKVCT 8  
DB 1 FCYWKVCT 8  
RESULT 7  
AAR05192  
ID AAR05192 standard; protein; 8 AA.  
XX  
XX AAR05192;  
XX  
XX 25-MAR-2003 (revised)  
XX 10-MAR-2003 (revised)  
XX 11-OCT-1990 (first entry)  
XX  
XX Somatostatin analogue or deriv. used as lung damage protectant.  
XX  
XX Somatostatin; lung damage protection; respiratory distress syndrome;  
XX oxygen therapy.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Disulfide-bond 2..7  
XX  
XX DE3937539-A.  
XX 31-MAY-1990.  
XX  
XX 10-NOV-1989; 89DE-03937539.  
XX  
XX 11-NOV-1988; 88DE-03838380.  
XX  
XX (SANO ) SANDOZ AG.  
XX  
XX Chrusasik J, Chrusasik S;  
XX WPI; 1990-172518/23.  
XX  
XX Somatostatin and its analogues or derivs. - used for protection against  
XX lung damage, esp. respiratory distress syndrome or damage caused by  
XX oxygen therapy.  
PT

XX Disclosure; Page 7; -pp; German.  
XX  
XX Residues A at positions 1 is beta-Naphthyl-(D)Alanine and residue Trp at  
XX position 4 is D-Trp. Derivs of this sequence subst. on the N-terminal  
XX amino gp. by N alpha-(alpha-glucosyl(1-4)deoxyfructosyl) or N alpha-(beta  
XX -deoxyfructosyl) are pref. for oral administration. The cpds. are esp.  
XX used to prevent, inhibit or treat respiratory distress syndrome in  
XX children and adults, and to inhibit or treat lung damage caused by oxygen  
XX therapy. Opt. they are formulated with a glucocorticoid steroid. The y  
XX are also known to inhibit release of growth hormone, insulin, and  
XX glucagon, and to reduce gastric secretions. See also AAR05177-80,  
XX AAR05182-88, AAR05191-95, AAR05197. (Updated on 10-MAR-2003  
XX to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 100.0%; Score 51; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 XCYWKVCT 8  
DB 1 ACYWKVCT 8  
RESULT 8  
AAR14234  
ID AAR14234 standard; protein; 8 AA.  
XX  
XX AAR14234;  
XX  
XX 25-MAR-2003 (revised)  
XX 18-DEC-1991 (first entry)  
XX  
XX Somatostatin deriv. #9 contg. cytotoxic moiety.  
XX  
XX pituitary growth hormone; GH; antineoplastic.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 1  
XX FT /label= OTHER  
XX FT /note= "D-Phe which carries 2,3-diaminopropionic acid(4-  
XX FT [bis(2-chloroethyl)amino]-Phe)2 cytotoxic moiety"  
XX FT Disulfide-bond 2..7  
XX  
XX EP450480-A.  
XX  
XX 09-OCT-1991.  
XX  
XX 27-MAR-1991; 91EP-00104845.  
XX  
XX 06-APR-1990; 90US-00505501.  
XX  
XX (TULA ) TULANE EDUCATIONAL FUND.  
XX (SCHA/) SCHALLY A V.  
XX  
XX Schally AV, Janaky T, Cai RZ;  
XX WPI; 1991-297292/41.  
XX  
XX New cyclic somatostatin peptide derivatives - have cytotoxic activity,  
XX used for treating certain cancers e.g. adeno and mammary carcinoma(s),  
XX gastric cancers, brain tumours, etc.  
XX  
XX Claim 9; Page 9 and Page 27; 28pp; English.  
XX  
XX The C-terminus is amidated and Phe(1) and Trp(4) are in the D-  
XX configuration. This peptide is a specific example of a generic formula.  
XX It inhibits secretion of pituitary GH and has neoplastic effect. It is  
XX useful for treatment of hormone-sensitive tumours. See AAR14225-R14238.  
CC

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CC      (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ      Sequence 8 AA;
XX
Query Match      100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 XCYWKVCT 8
       :|||||
Db      1 FCYWKVCT 8

RESULT 9
AAR14226
ID      AAR14226 standard; protein; 8 AA.
XX
AC      AAR14226;
XX
XX      25-MAR-2003 (revised)
DT      10-MAR-2003 (revised)
DT      09-APR-1991 (first entry)
XX
XX      Somatostatin deriv. #1 contg. cytotoxic moiety.
DE      pituitary growth hormone; GH; antineoplastic.
XX      Synthetic.
XX      Key
FH      Modified-site 1 Location/Qualifiers
FT      Disulfide-bond 2..7 /label= OTHER
FT      Disulfide-bond 2..7 /note= "4-Ibis(2-chloroethyl)amino]-Phe"
XX
XX      EP450480-A.
XX
XX      09-OCT-1991.
PD
XX      27-MAR-1991; 91EP-00104845.
PF
XX      06-APR-1990; 90US-00505501.
PR
XX      (TULANE ) TULANE EDUCATIONAL FUND.
PA      (SCHALL) SCHALL A V.
XX
XX      Schally AV, Janaky T, Cai RZ;
PI
XX      WPI; 1991-297292/41.
DR
XX      New cyclic somatostatin peptide derivatives - have cytotoxic activity,
PT      used for treating certain cancers e.g. adeno and mammary carcinoma(s),
PT      gastric cancers, brain tumours, etc.
XX
XX      Claim 7; Page 9 and Page 27; 28pp; English.
PS
XX      The C-terminus is amidated. This peptide is an example of a generic
XX      formula. It inhibits secretion of pituitary GH and has neoplastic effect.
CC      It is useful for treatment of hormone-sensitive tumours. See AAR14225-
CC      R14238. (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SQ      Sequence 8 AA;
XX
Query Match      100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 XCYWKVCT 8
       :|||||
Db      1 FCYWKVCT 8

RESULT 10
AAR10504

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ID      AAR10504 standard; protein; 8 AA.
XX
AC      AAR10504;
XX
XX      25-MAR-2003 (revised)
DT      10-MAR-2003 (revised)
DT      09-APR-1991 (first entry)
XX
XX      Somatostatin; luteinising hormone releasing hormone.
DE      Somatostatin analogue.
XX
XX      Sustained release peptide compsn; lactic acid; glycolic acid;
XX      somatostatin; luteinising hormone releasing hormone.
XX      Unidentified.
XX
XX      Key
FH      Modified-site 1..1 Location/Qualifiers
FT      Disulfide-bond 2..7 /label= Phe= D-Phe
FT      Modified-site 4..4 /label= Trp= D-Trp
XX
XX      GB2234169-A.
XX
XX      30-JAN-1991.
PD
XX      17-JUL-1990; 90GB-00015722.
PF
XX      28-JUL-1989; 89CH-00002829.
PR
XX      (DEBI-) DEBIOPHARM SA.
XX
XX      Orsolin P;
PI
XX      WPI; 1991-031530/05.
DR
XX      Sustained release pharmaceutical peptide compsn. prepn. - involves
XX      preheating and compressing mixt. of lactic acid glycolic acid copolymers
XX      with active substance pamoate, etc.
XX
XX      Claim 9; Page 12; 14pp; English.
PS
XX      This peptide is used as the active substance in a pharmaceutical compsn.
XX      for sustained release of somatostatin. It is mixed with a lactic
XX      acid/glycolic acid co-polymer. All components are in the form of
XX      microparticles and an injectable soln. is obt'd. See also AAR10501-03 and
XX      AAR10505-09. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
XX      on 25-MAR-2003 to correct PA field.)
XX
SQ      Sequence 8 AA;
XX
Query Match      100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 XCYWKVCT 8
       :|||||
Db      1 FCYWKVCT 8

RESULT 11
AAR26371
ID      AAR26371 standard; peptide; 8 AA.
XX
AC      AAR26371;
XX
XX      25-MAR-2003 (revised)
DT      10-FEB-1993 (first entry)
DT
XX      Somatostatin analogue.
DE
XX      Skin disease; melanoma; keratosis; basal cell epithelial pagetoid;
XX      basal cell carcinoma; non toxic.
KW

```

```

XX OS Synthetic.
XX FH Key
XX FT Misc-difference 1 Location/Qualifiers
XX FT Disulfide-bond 2..7 /note= "D-beta-naphthylalanine"
XX FT Misc-difference 4
XX FT Modified-site 8 /note= "D-Trp"
XX FT /note= "amidated"
XX PN WO9213554-A1.
XX PD 20-AUG-1992.
XX PF 07-FEB-1992; 92WO-US001027.
XX PR 08-FEB-1991; 91US-00652863.
XX PA (BIOM-) BIOMEASURE INC.
XX PI Bogden AE, Moreau J;
XX DR WPI, 1992-299754/36.
XX PT Anti-proliferative compsn. comprising somatostatin analogue - used to
XX PT treat benign and malignant proliferative skin diseases e.g. melanomas.
XX PS Claim 10; Page 16; 25pp; English.
XX CC The peptide is an example of a somatostatin analogue used to treat
XX CC melanomas and their malignant skin metastases (these express somatostatin
XX CC receptors), recurring keratosis, non-invasive basal cell epithelial
XX CC pagetoid and basal cell carcinoma. Peptides have 4 (pref. 6 or 7) amino
XX CC acids with at least 20 (pref. 50) percent homology with the core region
XX CC of somatostatin and has a D-Trp at position 4. See also AAR26367-74.
XX CC (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
   |||||
   |||||
Db 1 XCYWKVCT 8

RESULT 12
AAR26370
ID AAR26370 standard; peptide; 8 AA.
XX AC AAR26370;
XX DT 25-MAR-2003 (revised)
XX DT 10-FEB-1993 (first entry)
XX DE Somatostatin analogue.
XX KW Skin disease; melanoma; keratosis; basal cell epithelial pagetoid;
XX KW basal cell carcinoma; non toxic.
XX OS Synthetic.
XX FH Key
XX FT Misc-difference 1 Location/Qualifiers
XX FT Disulfide-bond 2..7 /note= "D-Phe"
XX FT Misc-difference 4
XX FT Modified-site 8 /note= "D-Trp"

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FT XX /note= "amidated"
FT PN WO9213554-A1.
FT PD 20-AUG-1992.
FT PF 07-FEB-1992; 92WO-US001027.
FT PR 08-FEB-1991; 91US-00652863.
FT PA (BIOM-) BIOMEASURE INC.
FT PI Bogden AE, Moreau J;
FT DR WPI, 1992-299754/36.
FT PT Anti-proliferative compsn. comprising somatostatin analogue - used to
FT PT treat benign and malignant proliferative skin diseases e.g. melanomas.
FT PS Claim 9; Page 15; 25pp; English.
FT CC The peptide is an example of a somatostatin analogue used to treat
FT CC melanomas and their malignant skin metastases (these express somatostatin
FT CC receptors), recurring keratosis, non-invasive basal cell epithelial
FT CC pagetoid and basal cell carcinoma. Peptides have 4 (pref. 6 or 7) amino
FT CC acids with at least 20 (pref. 50) percent homology with the core region
FT CC of somatostatin and has a D-Trp at position 4. See also AAR26367-74.
FT CC (Updated on 25-MAR-2003 to correct FN field.)
FT XX SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
   |||||
   |||||
Db 1 FCYWKVCT 8

RESULT 13
AAR27177
ID AAR27177 standard; peptide; 8 AA.
XX AC AAR27177;
XX DT 09-SEP-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX DE Somatostatin analogue tyrosine kinase inhibitor #1.
XX KW tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;
XX KW release of; growth hormone; insulin; glucagon; prolactin;
XX KW inhibit exopeptidase; inhibit tumour growth; tumour transformation.
XX OS Synthetic.
XX FH Key
XX FT Modified-site 1 Location/Qualifiers
XX FT Disulfide-bond 2..7 /note= "beta-aspartyl", where alpha-carboxy group forms
XX FT Misc-difference 4 amide with indoline"
XX FT Modified-site 8 /note= "D-form"
XX FT /note= "amidated"
XX PN EP505680-A1.
XX PD 30-SEP-1992.
XX PF 27-JAN-1992; 92EP-00101196.

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XX
PR 25-JAN-1991; 91HU-00000272.
XX
XX (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
XX
PI Keri G, Mezeo I, Horvath A, Vadasz Z, Tepian I, Balogh A;
PI Csuka O, Boekoenyi G, Szoeki B, Horvath J, Idei M, Seproedi J;
XX
XX WPI; 1992-325051/40.
XX
XX New octa:peptide or hepta:peptide somastatin analogues - as tyrosine
XX kinase inhibitors for treating tumours and psoriasis, and for regulating
XX hormone release.
XX
XX Claim 5; Page 30; 36pp; English.
XX
XX This peptide is a somatostatin analogue showing more advantageous and
XX selective pharmacological action than somatostatin. It has a structure
XX inhibiting the activity of exopeptidases. It can be used in medicaments
XX to inhibit tumour growth or the activity of tyrosine kinase enzymes
XX involved in tumour transformation. It is also useful for regulating the
XX release of growth hormone, insulin, glucagon and prolactin. It may also
XX be used to inhibit pathological processes such as psoriasis, elicited by
XX the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Revised record issued on 09-SEP-2004 : Correction to feature table key
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 51; DB 2; Length 8;
XX Best Local Similarity 87.5%; Pred. No. 1.7e+06;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 XCYWKVCT 8
XX :|||||
XX Db 1 DCYWKVCT 8
XX
XX RESULT 14
XX AAR27178
XX ID AAR27178 standard; peptide; 8 AA.
XX
XX AC AAR27178;
XX
XX DT 09-SEP-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX
XX DE Somatostatin analogue tyrosine kinase inhibitor #2.
XX KW tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;
XX release of; growth hormone; insulin; glucagon; prolactin;
XX inhibit exopeptidase; inhibit tumour growth; tumour transformation.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form"
XX FT Disulfide-bond 2. .7
XX FT Misc-difference 4 /note= "D-form"
XX FT Modified-site 8 /note= "amidated"
XX
XX EP505680-A1.
XX
XX PD 30-SEP-1992.
XX
XX PF 27-JAN-1992; 92EP-00101196.
XX
XX PR 25-JAN-1991; 91HU-00000272.

```

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XX
XX (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
XX
XX Keri G, Mezeo I, Horvath A, Vadasz Z, Tepian I, Balogh A;
XX Csuka O, Boekoenyi G, Szoeki B, Horvath J, Idei M, Seproedi J;
XX
XX WPI; 1992-325051/40.
XX
XX New octa:peptide or hepta:peptide somastatin analogues - as tyrosine
XX kinase inhibitors for treating tumours and psoriasis, and for regulating
XX hormone release.
XX
XX Claim 5; Page 30; 36pp; English.
XX
XX This peptide is a somatostatin analogue showing more advantageous and
XX selective pharmacological action than somatostatin. It has a structure
XX inhibiting the activity of exopeptidases. It can be used in medicaments
XX to inhibit tumour growth or the activity of tyrosine kinase enzymes
XX involved in tumour transformation. It is also useful for regulating the
XX release of growth hormone, insulin, glucagon and prolactin. It may also
XX be used to inhibit pathological processes such as psoriasis, elicited by
XX the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Revised record issued on 09-SEP-2004 : Correction to feature table key
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 51; DB 2; Length 8;
XX Best Local Similarity 87.5%; Pred. No. 1.7e+06;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 XCYWKVCT 8
XX :|||||
XX Db 1 FCYWKVCT 8
XX
XX RESULT 15
XX AAR27188
XX ID AAR27188 standard; peptide; 8 AA.
XX
XX AC AAR27188;
XX
XX DT 09-SEP-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX
XX DE Somatostatin analogue tyrosine kinase inhibitor #12.
XX KW tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;
XX release of; growth hormone; insulin; glucagon; prolactin;
XX inhibit exopeptidase; inhibit tumour growth; tumour transformation.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT Modified-site 1 /label= OTHER
XX FT Disulfide-bond 2. .7
XX FT Misc-difference 4 /note= "D-form"
XX FT Modified-site 8 /note= "amidated"
XX
XX EP505680-A1.
XX
XX PD 30-SEP-1992.
XX
XX PF 27-JAN-1992; 92EP-00101196.
XX
XX PR 25-JAN-1991; 91HU-00000272.

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PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.

XX Keri G, Mezei I, Horvath A, Vadasz Z, Tepian I, Balogh A;  
PI Csuka O, Boeckemyl G, Szoek B, Horvath J, Idei M, Szecedi J;  
XX WPI; 1992-325051/40.  
DR

PT New octa:peptide or hepta:peptide somastatin analogues - as tyrosine  
PT kinase inhibitors for treating tumours and psoriasis, and for regulating  
PT hormone release.

PS Example 11; Page 23; 36pp; English.

CC This peptide is a somatostatin analogue showing more advantageous and  
CC selective pharmacological action than somatostatin. It has a structure  
CC inhibiting the activity of exopeptidases. It can be used in medicaments  
CC to inhibit tumour growth or the activity of tyrosine kinase enzymes  
CC involved in tumour transformation. It is also useful for regulating the  
CC release of growth hormone, insulin, glucagon and prolactin. It may also  
CC be used to inhibit pathological processes such as psoriasis, elicited by  
CC the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to  
CC correct PN field.)

CC Revised record issued on 09-SEP-2004 : Correction to feature table key

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;

Best local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8

Db 1 XCYWKVCT 8

Search completed: November 18, 2004, 16:22:33  
Job time : 69 secs



Thu Nov 18 16:38:25 2004

seq1.rat

*Too open*

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:39 ; Search time 21 Seconds  
(without alignments)  
25.264 Million cell updates/sec

Title: SEQ1  
Perfect score: 51  
Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUG COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 51    | 100.0       | 8      | 1 US-08-286-748B-7  | Sequence 7, Appli  |
| 2          | 51    | 100.0       | 8      | 3 US-08-586-670A-13 | Sequence 13, Appli |
| 3          | 51    | 100.0       | 8      | 3 US-08-586-670A-14 | Sequence 11, Appli |
| 4          | 51    | 100.0       | 8      | 4 US-09-528-200-157 | Sequence 157, App  |
| 5          | 51    | 100.0       | 9      | 3 US-08-586-670A-11 | Sequence 11, Appli |
| 6          | 51    | 100.0       | 9      | 3 US-08-586-670A-15 | Sequence 15, Appli |
| 7          | 47    | 92.2        | 8      | 3 US-09-484-318-1   | Sequence 1, Appli  |
| 8          | 47    | 92.2        | 8      | 3 US-09-484-318-8   | Sequence 8, Appli  |
| 9          | 47    | 92.2        | 8      | 3 US-09-484-319-1   | Sequence 1, Appli  |
| 10         | 47    | 92.2        | 8      | 3 US-09-484-319-8   | Sequence 8, Appli  |
| 11         | 47    | 92.2        | 8      | 3 US-09-484-320-1   | Sequence 1, Appli  |
| 12         | 47    | 92.2        | 8      | 3 US-09-484-320-8   | Sequence 8, Appli  |
| 13         | 47    | 92.2        | 8      | 3 US-09-484-321-1   | Sequence 1, Appli  |
| 14         | 47    | 92.2        | 8      | 3 US-09-484-321-8   | Sequence 8, Appli  |
| 15         | 47    | 92.2        | 8      | 3 US-09-484-323-1   | Sequence 1, Appli  |
| 16         | 47    | 92.2        | 8      | 3 US-09-484-323-8   | Sequence 8, Appli  |
| 17         | 47    | 92.2        | 8      | 3 US-09-325-769-1   | Sequence 1, Appli  |
| 18         | 47    | 92.2        | 8      | 3 US-09-325-769-2   | Sequence 2, Appli  |
| 19         | 47    | 92.2        | 8      | 3 US-09-636-170-1   | Sequence 1, Appli  |
| 20         | 47    | 92.2        | 8      | 3 US-09-636-170-8   | Sequence 8, Appli  |
| 21         | 47    | 92.2        | 8      | 3 US-09-637-518-1   | Sequence 1, Appli  |
| 22         | 47    | 92.2        | 8      | 3 US-09-637-518-8   | Sequence 8, Appli  |
| 23         | 47    | 92.2        | 8      | 4 US-09-528-200-156 | Sequence 156, App  |
| 24         | 47    | 92.2        | 8      | 4 US-09-528-200-159 | Sequence 158, App  |
| 25         | 46    | 90.2        | 9      | 3 US-08-985-526-13  | Sequence 13, Appli |
| 26         | 46    | 90.2        | 33     | 2 US-08-671-487A-3  | Sequence 3, Appli  |
| 27         | 46    | 90.2        | 33     | 4 US-09-194-296-3   | Sequence 3, Appli  |

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|----|----|------|------|------------------------|--------------------|
| 28 | 46 | 90.2 | 34   | 3 US-08-985-526-15     | Sequence 15, Appli |
| 29 | 45 | 88.2 | 6    | 2 US-08-282-980B-8     | Sequence 8, Appli  |
| 30 | 45 | 88.2 | 6    | 3 US-08-931-095-5      | Sequence 5, Appli  |
| 31 | 45 | 88.2 | 6    | 4 US-09-528-200-195    | Sequence 195, App  |
| 32 | 45 | 88.2 | 8    | 4 US-09-528-200-158    | Sequence 158, App  |
| 33 | 43 | 84.3 | 9    | 3 US-08-586-670A-16    | Sequence 16, Appli |
| 34 | 41 | 80.4 | 8    | 3 US-08-586-670A-19    | Sequence 19, Appli |
| 35 | 41 | 80.4 | 5179 | 4 US-09-538-092-1258   | Sequence 1258, App |
| 36 | 39 | 76.5 | 386  | 4 US-09-252-091A-20990 | Sequence 20990, A  |
| 37 | 38 | 74.5 | 195  | 4 US-09-270-767-45424  | Sequence 45424, A  |
| 38 | 38 | 74.5 | 312  | 4 US-09-252-991A-18251 | Sequence 18251, A  |
| 39 | 37 | 72.5 | 6    | 1 US-07-902-935-2      | Sequence 2, Appli  |
| 40 | 37 | 72.5 | 6    | 2 US-08-465-764-3      | Sequence 3, Appli  |
| 41 | 37 | 72.5 | 6    | 2 US-08-470-932-2      | Sequence 2, Appli  |
| 42 | 37 | 72.5 | 6    | 2 US-08-467-025-2      | Sequence 2, Appli  |
| 43 | 37 | 72.5 | 6    | 2 US-08-347-197-3      | Sequence 3, Appli  |
| 44 | 37 | 72.5 | 6    | 3 US-08-931-095-22     | Sequence 22, Appli |
| 45 | 37 | 72.5 | 6    | 3 US-08-931-095-23     | Sequence 23, Appli |

ALIGNMENTS

RESULT 1  
US-08-286-748B-7  
Sequence 7, Application US/09286748B  
Patent No. 5759542  
GENERAL INFORMATION:  
APPLICANT: Victor Gurevich  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY  
OF DRUGS BY PLATELETS FOR THE TREATMENT OF  
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,748B  
FILING DATE: August 5, 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: J. Peter Faasse  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 04547/013001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: Xaa is D-Naphthylalanine  
US-08-286-748B-7  
Query Match 100.0%; Score 51; Length 8;  
Best Local Similarity Pred. No. 3.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8  
1 XCYWKVCT 8

## RESULT 2

US-08-586-670A-13  
Sequence 13, Application US/08586670A  
Patent No. 6241965  
GENERAL INFORMATION:  
APPLICANT: McBridge, William  
APPLICANT: Dean, Richard T.  
TITLE OF INVENTION: Somatostatin Derivatives  
TITLE OF INVENTION: And their Radiolabeled Products  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,670A  
FILING DATE: 22-APR-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6241965nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,385-DD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..4  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked  
OTHER INFORMATION: to DTPA; Ttp is in the D conformation;  
US-08-586-670A-13

## Query Match

Best Local Similarity 100.0%; Score 51; DB 3; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8  
1 XCYWKVCT 8

## RESULT 3

US-08-586-670A-14  
Sequence 14, Application US/08586670A  
Patent No. 6241965  
GENERAL INFORMATION:  
APPLICANT: McBridge, William  
APPLICANT: Dean, Richard T.  
TITLE OF INVENTION: Somatostatin Derivatives  
TITLE OF INVENTION: And their Radiolabeled Products  
NUMBER OF SEQUENCES: 23

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,670A  
FILING DATE: 22-APR-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6241965nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,385-DD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317

## INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

## NAME/KEY: Modified-site

LOCATION: 1..4  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked  
OTHER INFORMATION: to 2-ketoglutonyl; Ttp is in the D conformation;  
US-08-586-670A-14

## Query Match

Best Local Similarity 100.0%; Score 51; DB 3; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8  
1 XCYWKVCT 8

## RESULT 4

US-09-528-200-157  
Sequence 157, Application US/09528200  
Patent No. 6630570  
GENERAL INFORMATION:  
APPLICANT: LICHIA, KAI  
APPLICANT: BECKER, ANDREAS  
APPLICANT: SEMMLER, WOLFHARD  
APPLICANT: WEIDENMANN, BERTRAM  
APPLICANT: HESSENTIN, CARSTEN  
APPLICANT: VOLKMER-ENGERT, RUDOLF  
APPLICANT: SCHNEIDER-MERGNER, JENS  
APPLICANT: BHARGAVA, SARAH  
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA  
FILE REFERENCE: SCH-1731  
CURRENT APPLICATION NUMBER: US/09/528,200  
CURRENT FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: DE 199 17 713.9  
PRIOR FILING DATE: 1999-09-04  
NUMBER OF SEQ ID NOS: 196  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 157  
LENGTH: 8  
TYPE: PPT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-528-200-157

Query Match 100.0%; Score 51; DB 4; Length 8;  
Best Local Similarity 87.5%; Pred. No. 3.8e+05;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
DB 1 FCYWKVCT 8

## RESULT 5

US-08-586-670A-11  
Sequence 11, Application US/08586670A  
Patent No. 6241965  
GENERAL INFORMATION:  
APPLICANT: McBridge, William  
TITLE OF INVENTION: Somatostatin Derivatives  
TITLE OF INVENTION: And their Radiolabeled Products  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Wilcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,670A  
FILING DATE: 22-APR-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6241965nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,385-DD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..3  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "The Lys is linked to a BAT chelator  
OTHER INFORMATION: through the side chain nitrogen; Xaa is  
OTHER INFORMATION: D-naphthylalanine; the Cys sulfur is methylated;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5..8  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "The Trp residue is in the D conformation;  
OTHER INFORMATION: the Cys side chain sulfur is methylated;  
US-08-586-670A-11

Query Match 100.0%; Score 51; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
DB 2 XCYWKVCT 9

## RESULT 6

US-08-586-670A-15  
Sequence 15, Application US/08586670A  
Patent No. 6241965  
GENERAL INFORMATION:  
APPLICANT: McBridge, William  
TITLE OF INVENTION: Somatostatin Derivatives  
TITLE OF INVENTION: And their Radiolabeled Products  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Wilcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,670A  
FILING DATE: 22-APR-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6241965nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,385-DD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..3  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "Lys is linked to a BAT chelator  
OTHER INFORMATION: through the side chain nitrogen and to DTPA  
OTHER INFORMATION: at the N-terminus; Xaa is D-naphthylalanine;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3..8  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "The Trp residue is in the D conformation;  
OTHER INFORMATION: each of the Cys side chain sulfur atoms are  
OTHER INFORMATION: methylated;  
US-08-586-670A-15

Query Match 100.0%; Score 51; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
DB 2 XCYWKVCT 9

## RESULT 7

US-09-484-318-1  
Sequence 1, Application US/09484318

```
/ Patent No. 6180085
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NOVEL DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,318
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotide
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: This is D-phenylalanine
/ NAME/KEY: DISULFID
/ LOCATION: (2)..(7)
/ NAME/KEY: SITE
/ LOCATION: (4)
/ OTHER INFORMATION: This is D-tryptophan
/ NAME/KEY: SITE
/ LOCATION: (8)
/ OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-318-1
```

```
Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 XCYWKTCT 8
       :|||||
Db      1 FCYWKTCF 8
```

```
RESULT 8
US-09-484-318-8
/ Sequence 8, Application US/09484318
/ Patent No. 6180085
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NOVEL DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,318
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotate
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: This is D-phenylalanine
/ NAME/KEY: DISULFID
/ LOCATION: (2)..(7)
/ NAME/KEY: SITE
/ LOCATION: (4)
/ OTHER INFORMATION: This is D-tryptophan
US-09-484-318-8
```

```
Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
```

```
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      1 XCYWKTCT 8
       :|||||
Db      1 FCYWKTCF 8
```

```
RESULT 9
US-09-484-319-1
/ Sequence 1, Application US/09484319
/ Patent No. 6180086
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,319
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotide
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: This is D-phenylalanine
/ NAME/KEY: DISULFID
/ LOCATION: (2)..(7)
/ NAME/KEY: SITE
/ LOCATION: (4)
/ OTHER INFORMATION: This is D-tryptophan
/ NAME/KEY: SITE
/ LOCATION: (8)
/ OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-319-1
```

```
Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 XCYWKTCT 8
       :|||||
Db      1 FCYWKTCF 8
```

```
RESULT 10
US-09-484-319-8
/ Sequence 8, Application US/09484319
/ Patent No. 6180086
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,319
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotate
/ NAME/KEY: SITE
/ LOCATION: (1)
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OTHER INFORMATION: This is D-phenylalanine  
 NAME/KEY: DISULFID  
 LOCATION: (2)..(7)  
 NAME/KEY: SITE  
 LOCATION: (4)  
 OTHER INFORMATION: This is D-tryptophan  
 US-09-484-319-8

Query Match 92.2%; Score 47; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
 :|||||  
 Db 1 FCYWKTCCT 8

RESULT 11  
 US-09-484-320-1  
 Sequence 1, Application US/09484320  
 Patent No. 6180087  
 GENERAL INFORMATION:  
 APPLICANT: Achilefu, Samuel  
 APPLICANT: Rajagopalan, Raghavan  
 APPLICANT: Dorschow, Richard B  
 APPLICANT: Bugaj, Joseph E.  
 TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications  
 FILE REFERENCE: dnastring  
 CURRENT APPLICATION NUMBER: US/09/484,320  
 CURRENT FILING DATE: 2000-01-18  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Ocotrectide  
 NAME/KEY: SITE  
 LOCATION: (1)  
 OTHER INFORMATION: This is D-phenylalanine  
 NAME/KEY: DISULFID  
 LOCATION: (2)..(7)  
 NAME/KEY: SITE  
 LOCATION: (4)  
 OTHER INFORMATION: This is D-tryptophan  
 NAME/KEY: SITE  
 LOCATION: (8)  
 OTHER INFORMATION: This C-terminal residue ends with a hydroxyl  
 US-09-484-320-1

Query Match 92.2%; Score 47; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
 :|||||  
 Db 1 FCYWKTCCT 8

RESULT 12  
 US-09-484-320-8  
 Sequence 8, Application US/09484320  
 Patent No. 6180087  
 GENERAL INFORMATION:  
 APPLICANT: Achilefu, Samuel  
 APPLICANT: Rajagopalan, Raghavan  
 APPLICANT: Dorschow, Richard B  
 APPLICANT: Bugaj, Joseph E.  
 TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications  
 FILE REFERENCE: dnastring  
 CURRENT APPLICATION NUMBER: US/09/484,320  
 CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 8  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Ocotrectate  
 NAME/KEY: SITE  
 LOCATION: (1)  
 OTHER INFORMATION: This is D-phenylalanine  
 NAME/KEY: DISULFID  
 LOCATION: (2)..(7)  
 NAME/KEY: SITE  
 LOCATION: (4)  
 OTHER INFORMATION: This is D-tryptophan  
 US-09-484-320-8

Query Match 92.2%; Score 47; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
 :|||||  
 Db 1 FCYWKTCCT 8

RESULT 13  
 US-09-484-321-1  
 Sequence 1, Application US/09484321  
 Patent No. 6183726  
 GENERAL INFORMATION:  
 APPLICANT: Achilefu, Samuel  
 APPLICANT: Rajagopalan, Raghavan  
 APPLICANT: Dorschow, Richard B  
 APPLICANT: Bugaj, Joseph E.  
 TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES  
 FILE REFERENCE: DNA STRING  
 CURRENT APPLICATION NUMBER: US/09/484,321  
 CURRENT FILING DATE: 2000-01-18  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Ocotrectide  
 NAME/KEY: SITE  
 LOCATION: (1)  
 OTHER INFORMATION: This is D-phenylalanine  
 NAME/KEY: DISULFID  
 LOCATION: (2)..(7)  
 NAME/KEY: SITE  
 LOCATION: (4)  
 OTHER INFORMATION: This is D-tryptophan  
 NAME/KEY: SITE  
 LOCATION: (8)  
 OTHER INFORMATION: This C-terminal residue ends with a hydroxyl  
 US-09-484-321-1

Query Match 92.2%; Score 47; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
 :|||||  
 Db 1 FCYWKTCCT 8

RESULT 14  
 US-09-484-321-8  
 Sequence 8, Application US/09484321

```

; Patent No. 6183726
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorschow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,321
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octrectate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; US-09-484-321-8

```

```

Query Match      92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 XCYWKTCT 8
       : |||||
Db      1 FCYWKTCCT 8

```

```

RESULT 15
US-09-484-323-1
; Sequence 1, Application US/09484323
; Patent No. 6190641
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorschow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,323
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octrectide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; US-09-484-323-1

```

```

Query Match      92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;

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```

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      1 XCYWKTCT 8
       : |||||
Db      1 FCYWKTCCT 8

```

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Search completed: November 18, 2004, 16:21:19
Job time : 22 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:39 ; Search time 64 Seconds  
(without alignments)  
71.922 Million cell updates/sec

Title: SEQ1  
Perfect score: 51  
Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX  
Gapcp 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 44    | 86.3        | 468    | 2     | Q81619      |
| 2          | 42    | 82.4        | 107    | 2     | Q7P380      |
| 3          | 42    | 82.4        | 256    | 2     | Q7R3E2      |
| 4          | 42    | 82.4        | 493    | 1     | TNR8 RAT    |
| 5          | 42    | 82.4        | 498    | 1     | TNR8 MOUSE  |
| 6          | 42    | 82.4        | 826    | 2     | Q8B1U1      |
| 7          | 41    | 80.4        | 192    | 2     | Q99G02      |
| 8          | 41    | 80.4        | 192    | 2     | Q9E228      |
| 9          | 41    | 80.4        | 192    | 2     | Q91B09      |
| 10         | 41    | 80.4        | 192    | 2     | Q8V5C5      |
| 11         | 41    | 80.4        | 312    | 2     | Q83237      |
| 12         | 41    | 80.4        | 317    | 2     | Q8E982      |
| 13         | 41    | 80.4        | 317    | 2     | Q8E985      |
| 14         | 41    | 80.4        | 322    | 2     | Q8E219      |
| 15         | 41    | 80.4        | 338    | 2     | Q8YFA7      |
| 16         | 41    | 80.4        | 335    | 2     | Q8G212      |
| 17         | 41    | 80.4        | 622    | 2     | Q7P1X6      |
| 18         | 41    | 80.4        | 5179   | 1     | MUC2 HUMAN  |
| 19         | 40    | 78.4        | 117    | 2     | Q6G3K0      |
| 20         | 40    | 78.4        | 208    | 2     | Q6FRA0      |
| 21         | 40    | 78.4        | 475    | 2     | Q9UAT5      |
| 22         | 40    | 78.4        | 593    | 2     | Q6TLC6      |
| 23         | 40    | 78.4        | 593    | 2     | AAQ96728    |
| 24         | 40    | 78.4        | 646    | 2     | Q6TLC7      |
| 25         | 40    | 78.4        | 646    | 2     | AAQ96727    |
| 26         | 40    | 78.4        | 821    | 2     | Q966D4      |
| 27         | 39    | 76.5        | 310    | 2     | Q8FK92      |
| 28         | 39    | 76.5        | 313    | 2     | Q8PE59      |
| 29         | 39    | 76.5        | 315    | 2     | Q706P3      |
| 30         | 39    | 76.5        | 315    | 2     | CA92907     |
| 31         | 39    | 76.5        | 316    | 2     | Q8GQ67      |

|    |    |      |     |   |          |                     |
|----|----|------|-----|---|----------|---------------------|
| 32 | 39 | 76.5 | 323 | 2 | Q8KMR0   | Q8KMR0 campylobact  |
| 33 | 39 | 76.5 | 324 | 2 | Q6D9N8   | Q6D9N8 erwinia car  |
| 34 | 39 | 76.5 | 358 | 2 | Q6GR30   | Q6GR30 xenopus lae  |
| 35 | 39 | 76.5 | 452 | 2 | Q8CGA0   | Q8CGA0 mus musculu  |
| 36 | 39 | 76.5 | 743 | 2 | Q7N288   | Q7N288 photorhabdu  |
| 37 | 38 | 74.5 | 31  | 2 | Q9DEW1   | Q9DEW1 cocurnix co  |
| 38 | 38 | 74.5 | 381 | 2 | Q7CMF4   | Q7CMF4 bacillus an  |
| 39 | 38 | 74.5 | 391 | 2 | Q9X356   | Q9X356 bacillus an  |
| 40 | 38 | 74.5 | 381 | 2 | AAT2858  | AAT2858 bacillus    |
| 41 | 38 | 74.5 | 435 | 2 | Q8N117   | Q8N117 aspergillus  |
| 42 | 38 | 74.5 | 515 | 2 | Q7WY59   | Q7WY59 rhizobium l  |
| 43 | 38 | 74.5 | 767 | 2 | Q7ZV77   | Q7ZV77 brachydanto  |
| 44 | 38 | 74.5 | 767 | 2 | Q6TNV9   | Q6TNV9 brachydanto  |
| 45 | 38 | 74.5 | 767 | 2 | AAQ91220 | AAQ91220 brachydant |

## ALIGNMENTS

|             |  |                       |           |               |             |
|-------------|--|-----------------------|-----------|---------------|-------------|
| RESULT 1    |  |                       |           |               |             |
| ID          | Q81619   | PRELIMINARY;          | PRT;      | 468 AA.       |             |
| AC          | Q81619   |                       |           |               |             |
| DT          | 01-MAR-2003 (TREMBlrel. 23, Created)                                   |                       |           |               |             |
| DT          | 01-MAR-2003 (TREMBlrel. 23, Last sequence update)                      |                       |           |               |             |
| DT          | 01-OCT-2003 (TREMBlrel. 25, Last annotation update)                    |                       |           |               |             |
| DE          | Zic family transcription factor.                                       |                       |           |               |             |
| GN          | Name=HrzicN;   |                       |           |               |             |
| OS          | Halocynthia roretzi (Sea squirt).                                      |                       |           |               |             |
| OC          | Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;                 |                       |           |               |             |
| OC          | Stolidobranchia; Pyuridae; Halocynthia.                                |                       |           |               |             |
| OX          | NCBI_TaxID=7729;   |                       |           |               |             |
| RN          | [1]  |                       |           |               |             |
| RP          | SEQUENCE FROM N.A.   |                       |           |               |             |
| RX          | MEDLINE=22308874; PubMed=12421701;                                     |                       |           |               |             |
| RA          | Wada S., Saiga H.;   |                       |           |               |             |
| RT          | "HrzicN", a new Zic family gene of ascidians, plays essential roles in |                       |           |               |             |
| RL          | the neural tube and notochord development.";                           |                       |           |               |             |
| DR          | EMBL; AB092643; BAC23063.1; -.   |                       |           |               |             |
| DR          | HSSP; P08047; ISP2.  |                       |           |               |             |
| DR          | GO; GO:0005634; C:nucleus; IEA.  |                       |           |               |             |
| DR          | GO; GO:0003676; F:nucleic acid binding; IEA.                           |                       |           |               |             |
| DR          | GO; GO:0008270; F:zinc ion binding; IEA.                               |                       |           |               |             |
| DR          | InterPro; IPR007087; ZnF_C2H2.   |                       |           |               |             |
| DR          | Pfam; PF00096; ZF_C2H2; 4.   |                       |           |               |             |
| DR          | ProDom; PD000003; ZnF_C2H2; 1.   |                       |           |               |             |
| DR          | SMART; SM00355; ZnF_C2H2; 5.   |                       |           |               |             |
| DR          | PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.                               |                       |           |               |             |
| DR          | PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.                               |                       |           |               |             |
| SQ          | SEQUENCE 468 AA; 51632 MW; DB367B4A5C1FP31 CRG64;                      |                       |           |               |             |
| Query Match |  |                       |           |               |             |
|             |  | 86.3%;                | Score 44; | DB 2;         | Length 468; |
|             |  | Best Local Similarity | 75.0%;    | Pred. No. 32; |             |
| Matches     | 6;   | Conservative          | 1;        | Mismatches    | 1;          |
|             |  |                       |           | Indels        | 0;          |
|             |  |                       |           | Gaps          | 0;          |
| Qy          | 1 XCYWKVCT 8   |                       |           |               |             |
| Db          | 157 TCYWKDCT 164   |                       |           |               |             |
| RESULT 2    |  |                       |           |               |             |
| ID          | Q7P380   | PRELIMINARY;          | PRT;      | 107 AA.       |             |
| AC          | Q7P380;  |                       |           |               |             |
| DT          | 01-MAR-2004 (TREMBlrel. 26, Created)                                   |                       |           |               |             |
| DT          | 01-MAR-2004 (TREMBlrel. 26, Last sequence update)                      |                       |           |               |             |
| DT          | 01-MAR-2004 (TREMBlrel. 26, Last annotation update)                    |                       |           |               |             |
| DE          | ENSGANGP0000024086.  |                       |           |               |             |
| GN          | Name=ENSGANGP0000020752;   |                       |           |               |             |
| OS          | Anopheles gambiae str. PEST.   |                       |           |               |             |
| OC          | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;          |                       |           |               |             |
| OC          | Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.   |                       |           |               |             |

| QY                    | DB   | 1               | XCWKCVC 7 | Score 42; DB 2; Length 107;       | Indels 0; Gaps 0 |
|-----------------------|--|-----------------|-----------|-----------------------------------|------------------|
| QY                    | DB   | 1               | XCWKCVC 7 | Score 42; DB 2; Length 107;       | Indels 0; Gaps 0 |
| DB                    | 62   | DCFWKCVC 68     |           |                                   |                  |
| Query Match           |  |                 |           |                                   |                  |
| Best Local Similarity |  | 71.4%;          |           | Pred. No. 17;                     |                  |
| Matches               |  | 5; Conservative |           | 2; Mismatches 0; Indels 0; Gaps 0 |                  |
| RESULT 3              |  |                 |           |                                   |                  |
| ID                    | Q7R3E2   | PRELIMINARY;    |           | PRT; 256 AA.                      |                  |
| AC                    | Q7R3E2;  |                 |           |                                   |                  |
| DT                    | 01-MAR-2004 (TREMBLrel. 26, Created)   |                 |           |                                   |                  |
| DT                    | 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  |                 |           |                                   |                  |
| DT                    | 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  |                 |           |                                   |                  |
| DE                    | GLP 111 2064 2834.   |                 |           |                                   |                  |
| OS                    | Giardia lamblia ATCC 50803.  |                 |           |                                   |                  |
| OC                    | Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.   |                 |           |                                   |                  |
| OX                    | NCBI_TaxID=184922;   |                 |           |                                   |                  |
| RN                    | (1)  |                 |           |                                   |                  |
| RP                    | SEQUENCE FROM N.A.   |                 |           |                                   |                  |
| RC                    | STRAIN=WB C6;  |                 |           |                                   |                  |
| RA                    | Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;                             |                 |           |                                   |                  |
| RT                    | "Draft sequence of the Giardia lamblia genome.";   |                 |           |                                   |                  |
| RL                    | Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  |                 |           |                                   |                  |
| CC                    | -!- CAUTION: The sequence shown here is derived from an  |                 |           |                                   |                  |
| CC                    | EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is   |                 |           |                                   |                  |
| CC                    | preliminary data.  |                 |           |                                   |                  |
| DR                    | EMBL; AACB01000016; EAA41776.1; -  |                 |           |                                   |                  |
| SQ                    | SEQUENCE 107 AA; 11827 MW; EC738BD611F12DE5 CRC64;   |                 |           |                                   |                  |
| Query Match           |  |                 |           |                                   |                  |
| Best Local Similarity |  | 82.4%;          |           | Score 42; DB 2; Length 107;       |                  |
| Matches               |  | 5; Conservative |           | 2; Mismatches 0; Indels 0; Gaps 0 |                  |
| RESULT 4              |  |                 |           |                                   |                  |
| ID                    | TNR8 RAT   | STANDARD;       |           | PRT; 493 AA.                      |                  |
| AC                    | P97525;  |                 |           |                                   |                  |
| DT                    | 28-FEB-2003 (Rel. 41, Created)   |                 |           |                                   |                  |
| DT                    | 28-FEB-2003 (Rel. 41, Last sequence update)  |                 |           |                                   |                  |
| DT                    | 05-JUL-2004 (Rel. 44, Last annotation update)  |                 |           |                                   |                  |
| DE                    | Tumor necrosis factor receptor superfamily member 8 precursor (CD30L receptor) (Lymphocyte activation antigen CD30). |                 |           |                                   |                  |
| GN                    | Name="tnfrsf8; Synonyms=CD30;  |                 |           |                                   |                  |
| OS                    | Rattus norvegicus (Rat).   |                 |           |                                   |                  |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                 |           |                                   |                  |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  |                 |           |                                   |                  |
| OX                    | NCBI_TaxID=10116;  |                 |           |                                   |                  |
| RN                    | (1)  |                 |           |                                   |                  |
| RP                    | SEQUENCE FROM N.A.   |                 |           |                                   |                  |
| RC                    | STRAIN=MKAH; TISSUE=T-cell lymphoma;   |                 |           |                                   |                  |
| RC                    | MEDLINE=97136705; PubMed=6982082;  |                 |           |                                   |                  |
| RA                    | Aizawa S., Satoh H., Horie R., Ito K., Choi S.H., Takeuchi H.,   |                 |           |                                   |                  |

| Qy | Db | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 5 |
|----|----|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|
|----|----|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|



CC Name=Thrsf8;  
 CC Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=BA1B/C; TISSUE=splencocytes;  
 CC MEDLINE=96133967; PubMed=8543792;  
 CC Bowen M.A., Lee R.K., Miragiolotta G., Nam S.Y., Podack E.R.;  
 CC "Structure and expression of murine CD30 and its role in cytokine  
 CC production";  
 CC J. Immunol. 156:442-449 (1996).  
 CC -1- FUNCTION: Receptor for TNFSF8/CD30L. May play a role in the  
 CC regulation of cellular growth and transformation of activated  
 CC lymphoblasts. Regulates gene expression through activation of NF-  
 CC kappa-B (By similarity).  
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3 and TRAF5 (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -1- TISSUE SPECIFICITY: Detected in thymus and in activated  
 CC splenocytes.  
 CC -1- INDUCTION: By concanavalin A and pokeweed mitogen in splenocytes.  
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----  
 CC EMBL: U25416; AAA92887.1; -;  
 CC MGD: MGI:39908; Thrsf8.  
 CC InterPro: IPR001368; TNFR\_C6.  
 CC Pfam: PF00202; TNFR\_C6; 3.  
 CC SMART: SMO0208; TNFR\_3.  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 CC PROSITE: PS00652; TNFR\_NGFR\_2; 2.  
 CC KEGG: Glycopolyp; Receptor; Repeat; Signal; Transmembrane.  
 CC SIGNAL 1 18  
 CC CHAIN 19 498  
 CC FT DOMAIN 19 238  
 CC FT TRANSMEM 259 279  
 CC FT DOMAIN 280 498  
 CC FT REPEAT 28 66  
 CC FT REPEAT 68 106  
 CC FT REPEAT 107 150  
 CC FT DISULFID 29 44  
 CC FT DISULFID 45 58  
 CC FT DISULFID 48 65  
 CC FT DISULFID 69 81  
 CC FT DISULFID 84 97  
 CC FT DISULFID 107 121  
 CC FT DISULFID 128 146  
 CC FT CARBOHYD 156 156  
 CC FT CARBOHYD 183 183  
 CC FT CARBOHYD 229 229  
 CC SEQUENCE 498 AA; 53216 MW; 98CA2A05B38AFA71 CRC64;

Query Match 82.4%; Score 42; DB 1; Length 498;  
 Best Local Similarity 71.4%; Pred. No. 72;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 XCYWKTCT 7  
 Db 307 LCYWKAC 313

RESULT 6

OCSEIJI  
 ID OCSEIJI  
 AC OCSEIJI  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Periplasmic nitrate reductase.  
 GN Name=narX; OrderedLocustNames=SC0848;  
 OS Shewanella oneidensis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Shewanella.  
 CC NCBI\_TaxID=70863;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=NR-1;  
 CC MEDLINE=22297666; PubMed=12368813; DOI=10.1038/nbt749;  
 CC Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 CC Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,  
 CC Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,  
 CC Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,  
 CC Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,  
 CC White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impriali M.,  
 CC Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,  
 CC Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,  
 CC Venter J.C., Nelson K.H., Fraser C.M.,  
 CC "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 CC RT Shewanella oneidensis.";  
 CC Nat. Biotechnol. 20:1118-1123 (2002).  
 CC EMBL: AE015529; AAN53924.1; -;  
 CC HSSP: P81166; 2NAP.  
 CC TIGR: SC0848; -;  
 CC GO: GO:0005506; F:iron ion binding; IEA.  
 CC GO: GO:0030151; F:molybdenum ion binding; IEA.  
 CC GO: GO:0008940; E:nitrate reductase activity; IEA.  
 CC GO: GO:0016491; E:oxidoreductase activity; IEA.  
 CC GO: GO:0042128; E:nitrate assimilation; IEA.  
 CC InterPro: IPR009010; Asp decar fold.  
 CC InterPro: IPR006656; Molybdopterin.  
 CC InterPro: IPR006963; Molybdop\_Fe4S4.  
 CC InterPro: IPR006657; Mol\_dinuc\_bind.  
 CC InterPro: IPR010051; NAPA.  
 CC InterPro: IPR006311; Tat.  
 CC Pfam: PF00384; Molybdopterin; 1.  
 CC Pfam: PF04879; Molybdop\_Fe4S4; 1.  
 CC Pfam: PF01568; Molybdop\_Binding; 1.  
 CC TIGRPFAMs: TIGR01706; NAPA; 1.  
 CC TIGRPFAMs: TIGR01409; Tat\_signal\_seq; 1.  
 CC Complete proteome.  
 CC SEQUENCE 826 AA; 92474 MW; 33474D23868F6316 CRC64;

Query Match 82.4%; Score 42; DB 2; Length 826;  
 Best Local Similarity 62.5%; Pred. No. 1,le+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 XCYWKTCT 8  
 Db 473 NCYWTWCT 480

RESULT 7  
 ID OCSEIJI  
 AC OCSEIJI  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Helicoverpa armigera nucleopolyhedrovirus G4.  
 CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 CC Nucleopolyhedrovirus.  
 CC NCBI\_TaxID=148363;  
 CC [1]  
 CC SEQUENCE FROM N.A.

Query Match 82.4%; Score 42; DB 2; Length 826;  
 Best Local Similarity 62.5%; Pred. No. 1,le+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

RA Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
RT "Sequence analysis of the gp37 gene of Helicobacter armigera single-
RT nucleocapsid nucleopolyhedrovirus.";
RU Zhongguo Bing Du Xue 15:35-42(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
RT "Sequence analysis of the Iap3 gene of Helicobacter armigera single-
RT nucleocapsid nucleopolyhedrovirus.";
RU Zhongguo Bing Du Xue 15:43-49(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=21078302; PubMed=11210934;
RW Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
RT "Nucleotide sequence and transcriptional analysis of a putative basic
RT DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
RU Virus Genes 22:113-120(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=21064569; PubMed=11125177;
RW Chen X., Idkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
RA Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
RT "The sequence of the Helicoverpa armigera single-nucleocapsid
RT nucleopolyhedrovirus genome.";
RU J. Gen. Virol. 82:241-257(2001).
DR EMBL, AF271059; AAG53851.1; -.
KW Hypothetical protein.
SQ SEQUENCE 192 AA; 22773 MW; 941387892F8E8D1E CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
Db 60 NCHWKVC 66

RESULT 8
Q9E228 PRELIMINARY; PRT; 192 AA.
AC Q9E228;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RA Robertson A.P.S.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF275264; AAG17374.1; -.
KW Hypothetical protein.
SQ SEQUENCE 192 AA; 22747 MW; D5138789322580B5 CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
Db 60 NCHWKVC 66

RESULT 9
Q91B09 PRELIMINARY; PRT; 192 AA.
AC Q91B09;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Helicoverpa armigera nuclear polyhedrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=51313;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang C.X., Wu J.C.;
RT "Genome structure and the p10 gene of the Helicoverpa armigera
RT nucleopolyhedrovirus.";
RU Acta Biochim. Biophys. Sin. 33:179-184(2001).
DR EMBL, AF303045; AAK96351.1; -.
KW Hypothetical protein.
SQ SEQUENCE 192 AA; 22745 MW; 94138789371F641E CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
Db 60 NCHWKVC 66

RESULT 10
Q8V5Q5 PRELIMINARY; PRT; 192 AA.
AC Q8V5Q5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE ORF11.
OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21830929; PubMed=11842262;
RW Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
RA Presnail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M.;
RT "Comparative analysis of the complete genome sequences of Helicoverpa
RT zea and Helicoverpa armigera single-nucleocapsid
RT nucleopolyhedroviruses.";
RU J. Gen. Virol. 83:673-684(2002).
DR EMBL, AF334030; AAL56117.1; -.
KW Hypothetical protein.
SQ SEQUENCE 192 AA; 22675 MW; 549DBC848FEE8D CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
Db 60 NCHWKVC 66

RESULT 11
Q83Z37 PRELIMINARY; PRT; 312 AA.
AC Q83Z37;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR2R;

```

```

RA Kinschert T.G., Willis D.K.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY253670; AAPI4350.1; -.
DR InterPro: IPR011092; DUF1527.
DR Pfam: PF07513; DUF1527; 1.
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 33457 MW; 9C1A00C2B3FAE4 CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 312;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8
Db 48 ICYWLCT 55

RESULT 12
ID Q889B2 PRELIMINARY; PRT; 312 AA.
AC Q889B2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=PSPT00849;
OC Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RC MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buehl C.R., Joardar V., Lindeberg M., Sengupta J., Paulsen I.T.,
RA Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Duganthy S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uteerback T.R., Van Aken S.E., Feldlyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarewitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.J., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL: AE016858; AAO54384.1; -.
DR TIGR: PSP00849; -.
DR InterPro: IPR011092; DUF1527.
DR Pfam: PF07513; DUF1527; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 312 AA; 33422 MW; 1C91DBDBE3E40F CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 312;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8
Db 48 ICYWLCT 55

RESULT 13
ID Q6VSS5 PRELIMINARY; PRT; 317 AA.
AC Q6VSS5;
DT 01-OCT-2004 (TRENBLrel. 28, Created)
DT 01-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein yap154.
GN Name=yap154;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

```

```

OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=32777;
RA Collin F., Billaule A., Mullet C., Simonet M., Marceau M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: A627388; CAF28528.1; -.
KW Hypothetical protein.
SQ SEQUENCE 317 AA; 34498 MW; E3C6914F021AD1AC CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 317;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8
Db 49 ICYWLCT 56

RESULT 14
ID Q82119 PRELIMINARY; PRT; 322 AA.
AC Q82119; Q7C5F8;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein STY4576.
GN OrderedLocustNames=STY4576; t4273;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Parkhill J., Bentley K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Churcher C.M., Mungall K.L., Brooks K., Chillingworth T., Connor P.,
RA Baker S., Basham D., Davies P., Davies R.W., Doad L., White N., Farrar J.,
RA Cronin A., Davis P., Davies R.W., Doad L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Helgoyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RC MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blatterer F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL: AL627282; CAD09351.1; -.
DR EMBL: AE016848; AAO71731.1; -.
DR InterPro: IPR011092; DUF1527.
DR Pfam: PF07513; DUF1527; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 322 AA; 34841 MW; 8E08C95F19237648 CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 322;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8
Db 48 ICYWLCT 55

```

## RESULT 15

Q8YFA7 PRELIMINARY; PRT; 335 AA.  
 ID Q8YFA7  
 AC Q8YFA7;  
 DT 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE TRANSCRIPTIONAL REGULATOR, ARAC FAMILY.  
 GN OrderedLocustNames=BME11615;  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16M / ATCC 23456 / Biotype 1;  
 RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;  
 RA Dejevichio V.G., Kapatal V., Redkar R.J., Patra G., Mujar C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,  
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,  
 RA Selkov E., Elizer P.H., Hagius S., O'Callaghan D., Teleson J.-J.,  
 RA Haselkorn R., Kyriades N.C., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 Brucella melitensis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
 CC -! SIMILARITY: Contains 1 HTH arac/xy1s-type DNA-binding domain.  
 DR EMBL: AE009597; AAL52796.1; -.  
 DR PIR: A13453; A13453.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006385; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR009057; Homeodomain\_like.  
 DR InterPro: IPR000005; HTHARAC.  
 DR InterPro: IPR02818; Th1/Pfpr.  
 DR Pfam: PF01965; D1-1\_Pfpr; 1.  
 DR Pfam: PF00165; HTH\_ARAC; 2.  
 DR PRINTS: PR00032; HTHARAC.  
 DR SMART: SM00342; HTH\_ARAC; 1.  
 DR PROSITE: PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
 KW Complete proteome; DNA-binding; Transcription regulation.  
 SQ SEQUENCE 335 AA; 37076 MW; F6631F5237F38D6 CRC64;

Query Match 80.4%; Score 41; DB 2; Length 335;  
 Best Local Similarity 62.5%; Pred. No. 72;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
 :|:|:|:  
 Db 59 RCAMKICT 66

Search completed: November 18, 2004, 16:20:53  
 Job time : 67 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 ; Search time 37 seconds  
(without alignments)  
20.804 Million cell updates/sec

Title: SEQ1  
Perfect score: 51  
Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length DB | ID       | Description          |
|------------|-------|-------------|-----------|----------|----------------------|
| 1          | 42    | 82.4        | 493       | 2 JCS486 | membrane glycoprot   |
| 2          | 41    | 80.4        | 322       | 2 AF1031 | hypothetical prote   |
| 3          | 41    | 80.4        | 335       | 2 F83453 | transcription regu   |
| 4          | 41    | 80.4        | 3020      | 2 A43932 | mucin 2 precursor    |
| 5          | 40    | 78.4        | 475       | 2 T33943 | hypothetical prote   |
| 6          | 38    | 74.5        | 381       | 2 F59101 | hypothetical prote   |
| 7          | 38    | 74.5        | 1513      | 2 A54855 | hypothetical prote   |
| 8          | 38    | 74.5        | 1567      | 2 T00568 | hypothetical prote   |
| 9          | 37    | 72.5        | 12        | 1 UOGM2  | urotensin II - lon   |
| 10         | 37    | 72.5        | 12        | 2 J50423 | urotensin II - A pep |
| 11         | 37    | 72.5        | 12        | 2 S42765 | urotensin II - tel   |
| 12         | 37    | 72.5        | 12        | 2 U50424 | urotensin II - B pep |
| 13         | 37    | 72.5        | 13        | 2 PQ0445 | urotensin II - lau   |
| 14         | 37    | 72.5        | 83        | 2 S10706 | urotensin II - precu |
| 15         | 37    | 72.5        | 125       | 2 I50499 | urotensin II-gamma   |
| 16         | 37    | 72.5        | 125       | 2 I50498 | urotensin II-alpha   |
| 17         | 37    | 72.5        | 253       | 2 T47303 | hypothetical prote   |
| 18         | 37    | 72.5        | 765       | 2 T09574 | transport protein    |
| 19         | 37    | 72.5        | 1375      | 2 T17672 | probable DNA repai   |
| 20         | 36    | 70.6        | 451       | 2 F83793 | DNA-damage-inducib   |
| 21         | 36    | 70.6        | 627       | 2 B84482 | probable gag-prote   |
| 22         | 36    | 70.6        | 871       | 2 S68482 | probable membrane    |
| 23         | 36    | 70.6        | 1360      | 2 T12064 | DNA binding protei   |
| 24         | 35    | 68.6        | 69        | 2 A86779 | hypothetical prote   |
| 25         | 35    | 68.6        | 392       | 2 T46418 | hypothetical prote   |
| 26         | 35    | 68.6        | 306       | 2 A40679 | transcription enha   |
| 27         | 35    | 68.6        | 521       | 2 T38466 | probable NRAMF-fam   |
| 28         | 35    | 68.6        | 523       | 2 B40679 | transcription enha   |
| 29         | 35    | 68.6        | 654       | 2 AH2445 | hypothetical prote   |

|    |    |      |     |          |                    |
|----|----|------|-----|----------|--------------------|
| 30 | 34 | 66.7 | 87  | 2 T33285 | hypothetical prote |
| 31 | 34 | 66.7 | 100 | 2 A31201 | Gli-related finger |
| 32 | 34 | 66.7 | 104 | 2 S69756 | hypothetical prote |
| 33 | 34 | 66.7 | 140 | 2 T33284 | hypothetical prote |
| 34 | 34 | 66.7 | 212 | 2 C8785  | hypothetical prote |
| 35 | 34 | 66.7 | 281 | 2 C82547 | hypothetical prote |
| 36 | 34 | 66.7 | 370 | 2 T47131 | G-protein coupled  |
| 37 | 34 | 66.7 | 373 | 2 JCT289 | cytochrome d ubiq  |
| 38 | 34 | 66.7 | 379 | 1 B28940 | cytochrome d ubiq  |
| 39 | 34 | 66.7 | 379 | 2 A10591 | cytochrome d ubiq  |
| 40 | 34 | 66.7 | 379 | 2 A89725 | cytochrome d ubiq  |
| 41 | 34 | 66.7 | 379 | 2 B85576 | cytochrome d ubiq  |
| 42 | 34 | 66.7 | 421 | 2 T22969 | hypothetical prote |
| 43 | 34 | 66.7 | 426 | 2 T15285 | hypothetical prote |
| 44 | 34 | 66.7 | 511 | 2 A69369 | glutamate synthase |
| 45 | 34 | 66.7 | 529 | 2 C69280 | conserved hypothet |

#### ALIGNMENTS

##### RESULT 1

JCS486 membrane glycoprotein CD30 homolog precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004

C/Accession: JCS486

R/Alzawa, S.; Satoh, H.; Horie, R.; Ito, K.; Choi, S.H.; Takeuchi, H.; Watanabe, T.

Gene 182, 155-162, 1996

A/Title: Cloning and characterization of a cDNA for rat CD30 homolog and chromosomal assi

A/Reference number: JCS486; MUID:97136705; PMID:8982082

A/Contents: T cell

A/Accession: JCS486

A/Molecule type: mRNA

A/Residues: 1-493 <Alz>

A/Cross-references: UNIPROT:P97525; DBSP:D42117; NID:G1817523; PIDN:BAA07699.1; PID:4100f

C/Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog

F/1-16/Domain: signal sequence #status predicted <SIG>

F/19-493/Product: membrane glycoprotein CD30 homolog #status predicted <Mat>

F/278-304/Domain: transmembrane #status predicted <TM>

F/305-493/Domain: intracellular #status predicted <INT>

Query Match 82.4% Score 42; DB 2; Length 493;

Best Local Similarity 71.4% Pred. No. 22;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7

DB 303 LCVWKVC 309

##### RESULT 2

AF1031 hypothetical protein STY4576 [imported] - Salmonella enterica subsp. enterica serovar Typh

C/Species: Salmonella enterica subsp. enterica serovar Typh

C/Note: this species has also been called Salmonella typhi

C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C/Accession: AF1031

R/Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Cmenton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AF1031

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-322 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAM09351.1; PID:G16505351; GSPDB:GN00176

C/Genetics:

A/Gene: STY4576

Query Match 80.4% Score 41; DB 2; Length 322;  
 Best Local Similarity 62.5%; Pred. No. 22;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWVCT 8  
 DB 48 ICYWLMT 55

## RESULT 3

transcription regulator, arac family BMEI1615 [imported] - Brucella melitensis (strain 1

C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004

A:Accession: A13453

R:Delevecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,

; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: A13453

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-335 <XUP>

A:Cross-references: UNIPROT:Q8YFA7; GB:AE008917; PIDN:AAU52796.1; PID:G17983633; GSPDB:G

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI1615

A:Map position: 1

Query Match 80.4% Score 41; DB 2; Length 335;  
 Best Local Similarity 62.5%; Pred. No. 23;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWVCT 8  
 DB 59 RCAMWICT 66

## RESULT 4

mucin 2 precursor, intestinal - human (fragments)

N:Alternate names: mucin SMWC-41

C:Species: Homo sapiens (man)

C:Date: 10-Mar-1993 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004

A:Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329

R:Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.

J. Biol. Chem. 269, 2440-2446, 1994

A:Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the

A:Reference number: A49963; MUID:94132002; PMID:8300571

A:Accession: A49963

A:Molecule type: mRNA

A:Residues: 1-639 <GU1>

A:Cross-references: UNIPROT:Q02817; UNIPROT:Q14884; GB:I21998

R:Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.W.; Lagace, R.E.; Kim, Y.S.

J. Biol. Chem. 267, 21375-21383, 1992

A:Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstr

A:Reference number: A45106; MUID:93016075; PMID:1400449

A:Accession: A45106

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 626-1895 <GU2>

A:Cross-references: GB:M94131; NID:G186395; PIDN:AAA59163.1; PID:G186396

A:Note: Sequence extracted from NCBI backbone (NCBIP:116706)

A:Accession: B45106

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 2037-3020 <GU3>

A:Cross-references: GB:M94132; NID:G186397; PIDN:AAA59164.1; PID:G186398

A:Experimental source: colon

A:Note: Sequence extracted from NCBI backbone (NCBIP:116698)

R:Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.W

J. Clin. Invest. 88, 1005-1013, 1991

A:Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorpi

A:Reference number: A43932; MUID:91558717; PMID:1885763

A:Accession: A43932

A:Molecule type: DNA

A:Residues: 1343-1350, 'U', 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>

A:Cross-references: GB:M74027; NID:G188863; PIDN:AAA59875.1; PID:G188864

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIP:55749; NCBIP:55750)

R:Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.

J. Biol. Chem. 264, 6480-6487, 1989

A:Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and evidence

A:Reference number: A33532; MUID:89197956; PMID:2703501

A:Accession: B33532

A:Molecule type: mRNA

A:Residues: 1916-2193 <GU4>

A:Cross-references: GB:M22405; NID:G188873; PIDN:AAA6334.1; PID:G188874

A:Experimental source: intestine

R:Tany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.

J. Clin. Invest. 87, 77-82, 1991

A:Title: Human bronchus and intestine express the same mucin gene.

A:Reference number: A61257; MUID:91086481; PMID:1985113

A:Accession: A61257

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 'T', 1925-1948, 'TTS', 1952-1954 <UJN>

A:Experimental source: bronchus

R:Xu, G.; Huan, L.; Khatiri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner,

Biochem. Biophys. Res. Commun. 183, 821-828, 1992

A:Title: Human intestinal mucin-like protein (MIP) is homologous with rat MLP in the C-te

A:Reference number: PQ0328; MUID:92198477; PMID:1550588

A:Accession: PQ0328

A:Molecule type: mRNA

A:Residues: 2328-2468 <XUG>

A:Cross-references: GB:M6523

A:Experimental source: small intestine

A:Accession: PQ0329

A:Molecule type: protein

A:Residues: 2328-2342, 'K', 2344-2354 <XUG1>

C:Genetics:

A:Gene: GDB:MUC2

A:Cross-references: GDB:120203; OMIM:158370

A:Map position: 11p15.5-11p15.5

C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von v

C:Keywords: glycoprotein; intestine; tandem repeat

F:2766-2834/Domain: von Willebrand factor type C repeat homology <WVC>

Query Match 80.4% Score 41; DB 2; Length 3020;  
 Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWVCT 7  
 DB 1237 FCYWEIC 1243

## RESULT 5

hypothetical protein CO1B4.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

A:Accession: T33943

R:Smith, A.; Mamsley, P.; Fronick, W.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid CO1B4.

A:Reference number: 221443

A:Accession: T33943

A:Status: preliminary; translated from GB/EMBL/DBDB

A:Molecule type: DNA

A:Residues: 1-475 <SWI>

A:Cross-references: UNIPROT:Q9UAT5; EMBL:AF125352; PIDN:AAU44699.1; GSPDB:GN00023; CESP:G

A:Experimental source: strain Bristol N2; clone CO1B4

C:Genetics:

A:Gene: CESP:CO1B4.7

A:Map position: 5  
A:Introns: 45/2; 80/1; 118/2; 189/3; 239/2; 340/3; 433/3

Query Match 78.4%; Score 40; DB 2; Length 475;  
Best Local Similarity 83.3%; Pred. No. 43;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YMKVCT 8  
DB 264 YMKICT 269

RESULT 6

F59101  
hypothetical protein PX01-86 - Bacillus anthracis virulence plasmid pX01  
C:Species: Bacillus anthracis  
C>Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: F59101  
R:Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler  
J. Bacteriol. 181, 6509-6515, 1999  
A:Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harbored  
A:Reference number: A59091; MUID:99445483; PMID:10515943  
A:Accession: F59101  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-581 <OKI>  
A:Cross-references: UNIPROT:Q9X356; GB:A0605404; NID:64894216; PID:AA032390.1; PID:9489  
A:Experimental source: Strain Sterne  
A:Note: similar to hypothetical protein in BLTR-SpoIIIC intergenic region, Yrko B. subtl  
C:Genetics:  
A:Gene: PX01-86  
A:Genome: plasmid

Query Match 74.5%; Score 38; DB 2; Length 361;  
Best Local Similarity 83.3%; Pred. No. 74;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YMKVCT 8  
DB 340 YMKICT 345

RESULT 7

A54895  
mucin 2, intestinal/tracheal - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C:Accession: A54895  
R:Ohmori, H.; Dohman, A.F.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.; Kim, Y.S.; B  
J. Biol. Chem. 269, 17833-17840, 1994  
A:Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homolog  
A:Reference number: A54895; MUID:94299489; PMID:8027037  
A:Accession: A54895  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1513 <OHM>  
A:Cross-references: UNIPROT:Q62635; GB:U07615  
C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von  
C:Keywords: intestine

Query Match 74.5%; Score 38; DB 2; Length 1513;  
Best Local Similarity 57.1%; Pred. No. 2.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7  
DB 1234 FCTWCT 1240

RESULT 8

T00568  
hypothetical protein At2g39580 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F12L6.24

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: T00568; B84819  
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,  
submitted to the EMBL Data Library, July 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.  
A:Reference number: Z14168  
A:Accession: T00568  
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-1567 <ROU>  
A:Cross-references: UNIPROT:Q90645; EMBL:AC004218; NID:93355463; PID:93355487  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N  
M.; Xoo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.  
eues, D.; Nieman, M.C.; White, O.; Eisen, U.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: B84819  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1567 <STO>  
A:Cross-references: GB:A8002093; NID:93355487; PID:AA027849.1; GSPDB:GND0139  
C:Genetics:  
A:Gene: At2g39580; F12L6.24

A:Map position: 2  
A:Introns: 306/1; 346/3; 395/3; 688/1; 843/1; 945/3; 991/3; 1098/1  
C:Superfamily: Arabidopsis thaliana hypothetical protein F12L6.24

Query Match 74.5%; Score 38; DB 2; Length 1567;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7  
DB 1538 RCTWSLC 1544

RESULT 9

U00GM2  
urotensin II - long-jawed mudsucker  
C:Species: Gallitichthys mirabilis (long-jawed mudsucker)  
C>Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004  
C:Accession: A01409  
R:Pearson, D.; Shively, J.E.; Clark, B.R.; Geschwind, I.I.; Barkley, M.; Nishioka, R.; B  
Proc. Natl. Acad. Sci. U.S.A. 77, 5021-5024, 1980  
A:Title: Urotensin II: a somatostatin-like peptide in the caudal neurosecretory system o  
A:Reference number: A01409; MUID:81054904; PMID:6107911  
A:Accession: A01409  
A:Molecule type: protein  
A:Residues: 1-12 <PEA>  
A:Cross-references: UNIPROT:P01147  
A:Note: the proposed sequence was confirmed by synthesis of a peptide with the same stru  
C:Comment: Urotensin II is found in the teleost caudal neurosecretory system and is invo  
C:Superfamily: urotensin II  
C:Keywords: neuropeptide, osmoregulation  
F:6-11/Disulfide bonds: #status experimental

Query Match 72.5%; Score 37; DB 1; Length 12;  
Best Local Similarity 57.1%; Pred. No. 7.7;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7  
DB 5 DCFWKYC 11

RESULT 10

U00423  
urotensin II-A peptide - white sucker  
C:Species: Catostomus commersoni (white sucker)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

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Thu Nov 18 16:38:25 2004

seq1.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 ; Search time 139 Seconds  
(without alignments)  
20.381 Million cell updates/sec

Title: SEQ1  
Perfect score: 51  
Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                    | Description         |
|------------|-------|-------------|--------|-----------------------|---------------------|
| 1          | 47    | 92.2        | 8      | 9 US-09-781-980-6     | Sequence 22, Appl1  |
| 2          | 47    | 92.2        | 9      | 16 US-10-427-160A-22  | Sequence 66, Appl1  |
| 3          | 47    | 92.2        | 9      | 17 US-10-444-853A-515 | Sequence 515, Appl1 |
| 4          | 47    | 92.2        | 14     | 16 US-10-258-766A-1   | Sequence 1, Appl1   |
| 5          | 47    | 92.2        | 14     | 16 US-10-258-766A-7   | Sequence 6, Appl1   |
| 6          | 47    | 92.2        | 14     | 16 US-10-258-766A-7   | Sequence 7, Appl1   |
| 7          | 47    | 92.2        | 14     | 16 US-10-258-766A-8   | Sequence 8, Appl1   |
| 8          | 47    | 92.2        | 14     | 16 US-10-258-766A-13  | Sequence 13, Appl1  |
| 9          | 47    | 92.2        | 14     | 16 US-10-258-766A-14  | Sequence 14, Appl1  |
| 10         | 46    | 90.2        | 7      | 16 US-10-258-766A-5   | Sequence 5, Appl1   |
| 11         | 46    | 90.2        | 7      | 16 US-10-258-766A-10  | Sequence 10, Appl1  |
| 12         | 46    | 90.2        | 7      | 16 US-10-258-766A-12  | Sequence 12, Appl1  |
| 13         | 46    | 90.2        | 9      | 13 US-10-036-869-13   | Sequence 13, Appl1  |

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| 14 | 46 | 90.2 | 33   | 14 | US-10-300-083-3      | Sequence 3, Appl1      |
| 15 | 46 | 90.2 | 34   | 13 | US-10-036-869-15     | Sequence 15, Appl1     |
| 16 | 43 | 84.3 | 8    | 9  | US-09-781-980-5      | Sequence 5, Appl1      |
| 17 | 42 | 82.4 | 27   | 14 | US-10-058-053A-263   | Sequence 263, Appl1    |
| 18 | 42 | 82.4 | 27   | 16 | US-10-838-226-263    | Sequence 263, Appl1    |
| 19 | 42 | 82.4 | 78   | 14 | US-10-058-053A-38    | Sequence 38, Appl1     |
| 20 | 42 | 82.4 | 78   | 14 | US-10-058-053A-212   | Sequence 212, Appl1    |
| 21 | 42 | 82.4 | 78   | 16 | US-10-838-226-38     | Sequence 38, Appl1     |
| 22 | 42 | 82.4 | 78   | 16 | US-10-838-226-212    | Sequence 212, Appl1    |
| 23 | 42 | 82.4 | 275  | 16 | US-10-322-596-153    | Sequence 153, Appl1    |
| 24 | 41 | 80.4 | 21   | 14 | US-10-058-053A-234   | Sequence 234, Appl1    |
| 25 | 41 | 80.4 | 21   | 16 | US-10-838-226-234    | Sequence 234, Appl1    |
| 26 | 41 | 80.4 | 40   | 14 | US-10-058-053A-231   | Sequence 231, Appl1    |
| 27 | 41 | 80.4 | 40   | 14 | US-10-058-053A-264   | Sequence 264, Appl1    |
| 28 | 41 | 80.4 | 40   | 16 | US-10-838-226-231    | Sequence 231, Appl1    |
| 29 | 41 | 80.4 | 40   | 16 | US-10-838-226-264    | Sequence 264, Appl1    |
| 30 | 41 | 80.4 | 45   | 14 | US-10-058-053A-280   | Sequence 280, Appl1    |
| 31 | 41 | 80.4 | 45   | 16 | US-10-838-226-280    | Sequence 280, Appl1    |
| 32 | 41 | 80.4 | 90   | 14 | US-10-058-053A-80    | Sequence 80, Appl1     |
| 33 | 41 | 80.4 | 90   | 16 | US-10-838-226-80     | Sequence 80, Appl1     |
| 34 | 41 | 80.4 | 93   | 14 | US-10-058-053A-116   | Sequence 116, Appl1    |
| 35 | 41 | 80.4 | 93   | 16 | US-10-838-226-116    | Sequence 116, Appl1    |
| 36 | 41 | 80.4 | 95   | 14 | US-10-058-053A-89    | Sequence 89, Appl1     |
| 37 | 41 | 80.4 | 95   | 16 | US-10-838-226-89     | Sequence 89, Appl1     |
| 38 | 41 | 80.4 | 302  | 16 | US-10-437-963-152285 | Sequence 152285, Appl1 |
| 39 | 41 | 80.4 | 5179 | 9  | US-09-922-217-1068   | Sequence 1068, Appl1   |
| 40 | 41 | 80.4 | 5179 | 13 | US-09-833-263-1068   | Sequence 1068, Appl1   |
| 41 | 41 | 80.4 | 5179 | 13 | US-10-025-380-1068   | Sequence 1068, Appl1   |
| 42 | 41 | 80.4 | 5179 | 16 | US-10-734-384-121    | Sequence 121, Appl1    |
| 43 | 40 | 78.4 | 54   | 15 | US-10-424-599-254495 | Sequence 254495, Appl1 |
| 44 | 40 | 78.4 | 62   | 15 | US-10-424-599-212336 | Sequence 212336, Appl1 |
| 45 | 39 | 76.5 | 77   | 15 | US-10-424-599-218190 | Sequence 218190, Appl1 |

#### ALIGNMENTS

RESULT 1  
US-09-781-980-6  
Sequence 6, Application US/09781980  
Publication No. US20010029035A1  
GENERAL INFORMATION:  
APPLICANT: EISENHUT, MICHAEL  
APPLICANT: MIER, WALTER  
APPLICANT: ERITJA, RAMON  
APPLICANT: HABERKORN, UWE  
TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES  
FILE REFERENCE: 2502498.991110  
CURRENT APPLICATION NUMBER: US/09/781, 980  
CURRENT FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: DE 100 06 572  
PRIOR FILING DATE: 2000-02-14  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-781-980-6  
Query Match 92.2% ; Score 47 ; DB 9 ; Length 8 ;  
Best Local Similarity 75.0% ; Pred. No. 1.4e+06 ;  
Matches 6 ; Conservative 1 ; Mismatches 1 ; Gaps 0 ;

RESULT 2

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US-10-427-160A-22
; Sequence 22, Application US/10427160A
; Publication No. US20040110296A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Varscese, Chandra
; APPLICANT: Haeblerli, Peter
; APPLICANT: Wang, Weimin
; APPLICANT: Cheng, Tongqian
; TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery
; FILE REFERENCE: 600/032 (MBH02-312-A)
; CURRENT APPLICATION NUMBER: US/10/427,160A
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: PCT/US 02/15876
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/306,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 9
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; ORGANISM: Artificial Sequence
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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db      2 FCYWKTC 9

RESULT 3
US-10-444-953A-515
; Sequence 515, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haeblerli, Peter
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; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fornaugh, Kathy
; APPLICANT: Mokier, Victor
; APPLICANT: Jamison, Shaon
; APPLICANT: Walsh, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBH03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
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; SEQ ID NO 515
; LENGTH: 9
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; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Ser at position 1 is optionally present for coupling.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Phe at position 2 is optionally the D-isomer.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp at position 5 is optionally the D-isomer.
US-10-444-853A-515

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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db      2 FCYWKTC 9

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; Sequence 1, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthema, Inc.
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/ FILE REFERENCE: 717816.17
/ CURRENT APPLICATION NUMBER: US/10/258,766A
/ CURRENT FILING DATE: 2002-10-25
/ NUMBER OF SEQ ID NOS: 14
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/ LENGTH: 14
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/ OTHER INFORMATION: Cys(Acm)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (9)..(9)
/ OTHER INFORMATION: Tyr(OtBu)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: DTrp(tBoc)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)..(11)
/ OTHER INFORMATION: Lys(tBoc)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (12)..(12)
/ OTHER INFORMATION: Thr(OtBu)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (13)..(13)
/ OTHER INFORMATION: Cys(Acm)
/ NAME/KEY: MOD_RES
/ LOCATION: (14)..(14)
/ OTHER INFORMATION: Thr(OtBu)-O-RESIN
US-10-258-766A-1
```

```
Query Match      92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 XCYWKVCT 8
       :|||||
Db       7 FCYWKVCT 14
```

```
RESULT 5
US-10-258-766A-6
/ Sequence 6, Application US/10258766A
/ Publication No. US20040136907A1
/ GENERAL INFORMATION:
/ APPLICANT: Biosynthesa, Inc.
/ TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
/ FILE REFERENCE: 717816.17
/ CURRENT APPLICATION NUMBER: US/10/258,766A
/ CURRENT FILING DATE: 2002-10-25
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: DISULFID
/ LOCATION: (8)..(13)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(5)
/ OTHER INFORMATION: Amide bond between residues 1 and 5
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: DTrp
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (7)..(7)
/ OTHER INFORMATION: DPhc
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: DTrp
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (14)..(14)
/ OTHER INFORMATION: Thr-OH
US-10-258-766A-6
```

```
Query Match      92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 XCYWKVCT 8
       :|||||
Db       7 FCYWKVCT 14
```

```
RESULT 6
US-10-258-766A-7
/ Sequence 7, Application US/10258766A
/ Publication No. US20040136907A1
/ GENERAL INFORMATION:
/ APPLICANT: Biosynthesa, Inc.
/ TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
/ FILE REFERENCE: 717816.17
/ CURRENT APPLICATION NUMBER: US/10/258,766A
/ CURRENT FILING DATE: 2002-10-25
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: DISULFID
/ LOCATION: (8)..(13)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: MISC FEATURE
```

```
LOCATION: (1)..(5)
OTHER INFORMATION: Amide bond between residues 1 and 5
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)..(6)
OTHER INFORMATION: NH-DTPA
OTHER INFORMATION:
OTHER INFORMATION: Lys
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DpHe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr-OH
US-10-258-766A-7

Query Match          92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 7 FCYWKTCCT 14

RESULT 7
US-10-258-766A-8
Sequence 8, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
APPLICANT: Biosynthema, Inc.
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
FILE REFERENCE: 717816.17
CURRENT APPLICATION NUMBER: US/10/258,766A
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Arg(Pmc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr(OcBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
OTHER INFORMATION: Asp(beta-OAl1)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)..(6)
OTHER INFORMATION: Lys(Mct)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DpHe
FEATURE:
NAME/KEY: MOD_RES
```

```
LOCATION: (8)..(8)
OTHER INFORMATION: Cys(Acm)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9)..(9)
OTHER INFORMATION: Tyr(OcBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp(tBoc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: Lys(tBoc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (12)..(12)
OTHER INFORMATION: Thr(OcBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (13)..(13)
OTHER INFORMATION: Cys(Acm)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr(Ol)(OcBu)-O-RESIN
US-10-258-766A-8

Query Match          92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 7 FCYWKTCCT 14

RESULT 8
US-10-258-766A-13
Sequence 13, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
APPLICANT: Biosynthema, Inc.
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
FILE REFERENCE: 717816.17
CURRENT APPLICATION NUMBER: US/10/258,766A
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DpHe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr(Ol)-OH
FEATURE:
NAME/KEY: DISULFID
LOCATION: (8)..(13)
OTHER INFORMATION:
```

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FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(5)  
OTHER INFORMATION: Amide bond between residues 1 and 5  
US-10-258-766A-13

Query Match 92.2%; Score 47; DB 16; Length 14;  
Best Local Similarity 75.0%; Pred. No. 2.3;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
:|||||  
Db 7 FCYWKTC 14

RESULT 9  
US-10-258-766A-14  
Sequence 14, Application US/10258766A  
Publication No. US20040136907A1  
GENERAL INFORMATION:  
APPLICANT: Biosynthema, Inc.  
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES  
FILE REFERENCE: 717816.17  
CURRENT APPLICATION NUMBER: US/10/258,766A  
CURRENT FILING DATE: 2002-10-25  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4)..(4)  
OTHER INFORMATION: DTYr  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (6)..(6)  
OTHER INFORMATION: NH-DTPA  
OTHER INFORMATION: Lys  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (7)..(7)  
OTHER INFORMATION: DPhe  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (10)..(10)  
OTHER INFORMATION: DTrp  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (14)..(14)  
OTHER INFORMATION: Thr(Ol)-OH  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(5)  
OTHER INFORMATION: Amide bond between residues 1 and 5  
US-10-258-766A-14

Query Match 92.2%; Score 47; DB 16; Length 14;  
Best Local Similarity 75.0%; Pred. No. 2.3;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
:|||||  
Db 7 FCYWKTC 14

RESULT 10

US-10-258-766A-5  
Sequence 5, Application US/10258766A  
Publication No. US20040136907A1  
GENERAL INFORMATION:  
APPLICANT: Biosynthema, Inc.  
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES  
FILE REFERENCE: 717816.17  
CURRENT APPLICATION NUMBER: US/10/258,766A  
CURRENT FILING DATE: 2002-10-25  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DISULFID  
LOCATION: (1)..(6)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: Cys(Acm)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (2)..(2)  
OTHER INFORMATION: Tyr(OcBu)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (3)..(3)  
OTHER INFORMATION: DTrp(tBoc)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4)..(4)  
OTHER INFORMATION: Lys(tBoc)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: Thr(OcBu)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (6)..(6)  
OTHER INFORMATION: Cys(Acm)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (7)..(7)  
OTHER INFORMATION: Thr(OcBu)-O-RESIN  
US-10-258-766A-5

Query Match 90.2%; Score 46; DB 16; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYWKVCT 8  
:|||||  
Db 1 CYWKTC 7

RESULT 11  
US-10-258-766A-10  
Sequence 10, Application US/10258766A  
Publication No. US20040136907A1  
GENERAL INFORMATION:  
APPLICANT: Biosynthema, Inc.  
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES  
FILE REFERENCE: 717816.17  
CURRENT APPLICATION NUMBER: US/10/258,766A  
CURRENT FILING DATE: 2002-10-25  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 7  
TYPE: PRT

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ORGANISM: Homo sapiens
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (1)..(1)
  OTHER INFORMATION: Cys (AcM)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (2)..(2)
  OTHER INFORMATION: Tyr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (3)..(3)
  OTHER INFORMATION: DTrp (tBoc)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (4)..(4)
  OTHER INFORMATION: Lys (tBoc)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (5)..(5)
  OTHER INFORMATION: Thr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (6)..(6)
  OTHER INFORMATION: Cys (AcM)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (7)..(7)
  OTHER INFORMATION: Thr (OL) (OCBu) -O-RESIN
US-10-258-766A-10
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Query Match 90.2%; Score 46; DB 16; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYWKTCT 8  
DB 1 CYWKTCT 7

## RESULT 12

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US-10-258-766A-12
Sequence 12, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
  APPLICANT: Biosynhema, Inc.
  TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
  FILE REFERENCE: 717816.17
  CURRENT APPLICATION NUMBER: US/10/258,766A
  CURRENT FILING DATE: 2002-10-25
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 12
  LENGTH: 7
  TYPE: PRT
  ORGANISM: Homo sapiens
FEATURE:
  NAME/KEY: DISULFID
  LOCATION: (1)..(6)
  OTHER INFORMATION:
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (1)..(1)
  OTHER INFORMATION: Cys (AcM)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (2)..(2)
  OTHER INFORMATION: Tyr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (3)..(3)
  OTHER INFORMATION: DTrp (tBoc)
FEATURE:
```

```
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: Lys (tBoc)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (5)..(5)
  OTHER INFORMATION: Thr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (6)..(6)
  OTHER INFORMATION: Cys (AcM)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (7)..(7)
  OTHER INFORMATION: Thr (OL) (OCBu) -O-RESIN
US-10-258-766A-12
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Query Match 90.2%; Score 46; DB 16; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYWKTCT 8  
DB 1 CYWKTCT 7

## RESULT 13

```
US-10-036-869-13
Sequence 13, Application US/10036869
Publication No. US20020151516A1
GENERAL INFORMATION:
  APPLICANT: Mixson, James A
  TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
  ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
  THERAPY
  NUMBER OF SEQUENCES: 43
  CORRESPONDENCE ADDRESS:
  ADDRESS: Connelly, Bove, Lodge, & Hutz
  STREET: 1220 Market Street, P.O. Box 2207
  CITY: Wilmington
  STATE: Delaware
  COUNTRY: U.S.A.
  ZIP: 19899
  COMPUTER READABLE FORM:
  MEDIUM TYPE: floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/036,869
  FILING DATE: 29-Nov. US20020151516A1-2001
  CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/385,526
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 08/608,845
  FILING DATE: 16-JUL-1996
  ATTORNEY/AGENT INFORMATION:
  NAME: McMorow Jr., Robert G
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (302) 658-9141
  TELEFAX: (302) 658-5613
  INFORMATION FOR SEQ ID NO: 13:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 9 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-036-869-13
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Query Match 90.2%; Score 46; DB 13; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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seq1.rapb

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QY 1 XCYWKC 7  
:|||||  
Db 2 FCYWKC 8

RESULT 14

US-10-300-083-3

; Sequence 3, Application US/10300083  
; Publication No. US20030153502A1

; GENERAL INFORMATION:

; APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA  
; TITLE OF INVENTION: SYNTHETIC APPROACH TO DESIGNED CHEMICAL  
; STRUCTURES

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: MEETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
; STREET: 119 No. US20030153502A1th Fourth Street, Suite 203

; City: Minneapolis

; STATE: Minnesota

; COUNTRY: U.S.A.

; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/300,083

; FILING DATE: 20-No. US20030153502A1-2002

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/09/194,296

; FILING DATE: 15-Oct-1999

; APPLICATION NUMBER: US 08/653,632

; FILING DATE: 24-MAY-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MCCORMACK, MYRA M.

; REGISTRATION NUMBER: 36,602

; REFERENCE/DOCKET NUMBER: 110,00330220

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-305-1225

; TELEFAX: 612-305-1228

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-300-083-3

Query Match 90.2%; Score 46; DB 14; Length 33;

Best Local Similarity 85.7%; Pred. No. 6.4;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKC 7

:|||||

Db 12 FCYWKC 18

RESULT 15

US-10-036-869-15

; Sequence 15, Application US/10036869

; Publication No. US20020151516A1

; GENERAL INFORMATION:

; APPLICANT: Mixson, James A

; TITLE OF INVENTION: CARRIER DNA COMPLEXES CONTAINING DNA

; ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE

; THERAPY

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
; STREET: 1220 Market Street, P.O. Box 2207  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: U.S.A.

; ZIP: 19899

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/036,869

; FILING DATE: 29-No. US20020151516A1-2001

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/608,845

; FILING DATE: 16-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: McMorow Jr., Robert G

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 658-5613

; TELEFAX: (302) 658-5613

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-10-036-869-15

Query Match 90.2%; Score 46; DB 13; Length 34;

Best Local Similarity 85.7%; Pred. No. 6.5;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKC 7

:|||||

Db 2 FCYWKC 8

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Team: OIPEScanning

Dossier: 10021002

Legal Date: 10-14-2004

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Total number of pages: 44

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